

STIC Search Report Biotech-Chem Library

STIC Database Tracking Number 103553

TO: Sharon Turner

Location: CM1/10B09&10B19

Art Unit: 1647

Friday, September 12, 2003

Case Serial Number: 09/978191

From: P. Sheppard

Location: Biotech-Chem Library

CM1-1E03

Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes	7		
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STIC-Biotech/ChemLib

From: Sent: To:

Subject:

Turner, Sharon

Wednesday, September 10, 2003 1:19 PM STIC-Biotech/ChemLib 09978191

RECENTED

SEP 10 2003

.ECH/CHEM. DIVISION (STIC)

Please search CDB and interference files

AA SEQ ID NO:506

Sharon L. Turner, Ph.D. USPTO CM1-10B09 Mailroom 10B19 Biotechnology GAU 1647 (703) 308-0056

> Point of Contact P. Sheppard Telephone number: (703) 308-4499

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed: 4/12/03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other

VENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
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Other (specify):

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Q9uhf1 homo sapien
Q9uhf1 homo sapien
Q9qxt5 mus musculu
Q9dcp5 mus musculu
Q9dcp5 mus musculu
Q9jkw3 rattus norv
Q35447 mus musculu
Q99944 homo sapien
Q8iv30 homo sapien
Q9vzd0 drosophila
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61 ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP 120	1 MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR 60	1 MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR 60	Query Match 100.0%; Score 1505; DB 4; Length 273; Best Local Similarity 100.0%; Pred. No. 1.5e-127; Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	EGF-like domain. SEQUENCE 273 AA; 29631 MW; 5AD0A4845ED5B688 CRC64;	PS01187;	PROSITE: PS00022; EGF 1; 1.	PS00010;		IPR006209;	IPR001881;	InterPro; IPR000152; Asx hydroxyl.		J.R. ;	vary;	SEQUENCE FROM N.A.	[1]		Bunalyota; metazoa; thoraata; traniata; vertebrata; Eutereoscomi; Mammalja: Butherja: Primates: Catarrhini: Hominidae: Homo). ·	Similar to NEUl protein.	23, Last annotation	(TrEMBLrel. 19,	01-DEC-2001 (TrEMBLrel. 19, Created)	OSEGO PRELIMINARY; PRT; 273 AA.	1

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Koehrer K., Beyer A., Mewes H.W., Ga Submitted (DEC-2000) to the EMBL/Ger EMBL; AF186111; AAF014291; ---
EMBL; AF186111; AAF014291; ---
EMBL; AL512735; CAC21666.1; ---
HSSP; PO8709; IFAK. ASX hydroxyl. InterPro; IPR000125; ASX hydroxyl. InterPro; IPR001629; EGF_1ike. InterPro; IPR006209; EGF_1ike. Fam; PF00008; EGF; 2.
SMART; SM00179; EGF CA; 1.
PROSITE; PS00101; ASX HYDROXYL; 1.
PROSITE; PS01186; EGF_1; 1.
PROSITE; PS01187; EGF_CA; 1.
HYDCOTHER; PS01187; EGF_CA; 1.
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TISSUE=Uterus;
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                                    GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                             GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWBGHSLSADGTLCVPKG
                                                                                                                                                                                         ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                GPPRVAPNPTGVDSANKBEVQRLQSRVDLLEBKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                        GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                 ACSTYRTI YRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAI COPPCRNGGSCVQP
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P., Jelinek
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EMBL/GenBank/DDBJ
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Pred. No. 1.8e-127;
1; Mismatches 0;
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Best Local
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PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
EGF-like domain.
SEQUENCE 278 AA; 30125 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001881; EINTERPro; IPR006209; EINTERPro; IPR006210; IPF00008; EGF; 2.
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Q9QXT5;
Q1-MAY-2000 (TrEMBLrel
01-MAY-2000 (TrEMBLrel
01-MAR-2003 (TrEMBLrel
NOTCH4-like protein (V
VEZFI OR ZNEUI)
Mus musculus (Mouse)
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Martinez T
Submitted
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Submitted (M
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O'Hara P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Fammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                          Local
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                                                                                                                                                                                                                                                                                                                                                                       213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00181; EGF;
LLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKD
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                          GGPPRVAPNPT-GVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGS
                                                                                                                                                                                                                          RACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQ
                                                EGPSPVAPNPTAGVDSMAREEVYRLQARVDVLEQKLQLVLAPLHSLASRSTEHGLQDPGS
                                                                                                                           PGHCRCPVGWQGDTCQTDVDECSTGEASCPQRCVNTVGSYWCQGWEGQSPSADGTRCLSK
                                                                                                                                               PGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPK
                                                                                                                                                                                                    RACSTYRTIYRTAYRRSPGVTÞARÞRYACCÞGWKRTSGLÞGACGAAICQÞÞCGNGGSCIR
                                                                                                                                                                                                                                                                            MWGSGELLVAWFLVĹAADGTTEHVYRPSRRVCTVGISGGSISETFVQRVYQPYLTTCDGH
                                                                                                                                                                                                                                                                                                     MRGSQEVILMWILLVLAVGG-TEHAYRPGRRVCAYRAHGDPVSESFVQRVYQPFLTTCDGH
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z T., Hoffman
ed (SEP-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROM N.A.
P., Jelinek L.,
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                                                                                                                                                                                                                                                                                                                                                         78.4%; Score 1180; DB 11; larity 77.7%; Pred. No. 2.9e-98; Conservative 19; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) (TrEMBLrel. 13, Cre
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e protein (Vascular e
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Hoffman
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                                                                                                                                                                                                                                                                                                                                                                                                                                          30125 MW;
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EGF_like.
IEGF.
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the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
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Last annotation update)
Last endothelial zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                      863159F567102FA7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lehner
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; Murinae; Mus
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SEQUENCE FR Sheppard P. O'Hara P.; Submitted (

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Query Match Best Local S Matches 272

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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Garriboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Wordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y., Storch K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                              PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9DCP5;
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1313291; Vezf1.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like..
InterPro; IPR006210; IEGF.
Pfam; PF00008; EGF; 2.
SMART; SM00181; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001
01-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P00740; 1EDM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AK002601; BAB22222.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vascular
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                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                       PS00022; EGF 1; 1.
PS01186; EGF 2; 1.
                                                                                                                                                                                                             MRGSQEVILMWILLVLAVGG-TEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGH
 EGPSPVAPNPTAGVDSMAREEVYRLQARVDVLEQKLQLVLAPLHSLASRSTEHGLQDPGS
               GGPPRVAPNPT-GVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGS
                                                                PGHCRCPVGWQGDTCQTDVDECSTGEASCPQRCVNTVGSYWCQGWEGQSPSADGTRCLSK
                                                                                    PGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPK
                                                                                                                             RACSTYRTIYRTAYRRSPGVTPARPRYACCPGWKRTSGLPGACGAAICQPPCGNGGSCIR
                                                                                                                                                RACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQ
                                                                                                                                                                                             MWGSGELLVAWFLVLAADGTTEHVYRPSRRVCTVGISGGSISETFVQRVYQPYLTTCDGH
                                                                                                                                                                                                                                                                                                                                                   PS01186; EGF_2; 1.
PS01187; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     001 (TrEMBLrel. 1003 (TrEMBLrel. 2003 endothelial zinc
                                                                                                                                                                                                                                                                                                                             265 AA;
                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                             28665 MW;
                                                                                                                                                                                                                                                                           73.3%;
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. 17, Last sequence (
. 23, Last annotation
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                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                           Score 1103.5;
Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                             D81EC3DA884FF97E CRC64;
                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     annotation update)
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                                                                                                                                                                                                                                                                                            DB 11;
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                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                         Length
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Q9JKW3
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Best Local :
                                                                                         035447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISUE=Spleen;
Chan M.T.W., Ng C.C.Y., Lim E.K.B.,
Chan M.T.W., Ng C.C.Y., Lim E.K.B.,
"Cloning and Characterization of a "
protein in the Rat Spleen.";
Submitted (FEB-2000) to the EMBL/Ge
                                           01-JAN-1998 (TrEMBLrel. 05, Cr
01-JAN-1998 (TrEMBLrel. 05, La
01-MAR-2003 (TrEMBLrel. 23, La
Hypothetical 32.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9JKW3;
                                                                                                                                                                                                                                                                                                                                                              PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00008; EGF; 2.
SMART; SM00179; EGF_CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF223678; AAF35352.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marcantonio D., Huynh H.T.;
Submitted (JAN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001881; EGF_Ca.
                                                                                                                                                                                                                                                                                                                                                                                                                                            nterPro;
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                                                                                                                                                                                                            . 81
                                                                                                                                                                                                                                                                                                      130;
                                                                                                                                                                                                                                                        21
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                           EGHSLSADGTLCVPKGGPPRVAPNPT-GVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHS
                                                                                                                                                                                LASQALEHGLPDPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKD
                                                                                                                                                                                                            EGOSPSADGVLCLPKEGPSPVAPSPTPGVDSVVREXVYKLQARVDVLEQKLQLVLAPLHS
                                                                                                                                                                                                                                                                             AICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCW 164
                                                                                                                                                                                                                                                                                                                                                                                                            PS00010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKD
                                                                                                                                                              LASRSPEHGLQDPGSLLAHSFQQLDRIDSLSEQVSFLEEQLGSCSCKKD
                                                                                                                                                                                                                                                       AICOPPCGNEGSCIREGRCRCPVGWQGDTCQIDVDECSTGEARCPQRCVNTVGSYWCQCW
                                                                                                                                                                                                                                                                                                                                                                                     PS01186;
                                                                                                                                                                                                                                                                                                                                                                                                PS00022;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR006209;
                                                                                                                                                                                                                                                                                                                                                  190 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                    ; ASX HYDROXYL;
; EGF_1; 1.
; EGF_2; 1.
; EGF_CA; 1.
            Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                20527 MW;
                                                                                                                                                                                                                                                                                                    48.3%; Score 727.5; DB 1
76.9%; Pred. No. 1.1e-57;
tive 15; Mismatches 23
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15,
23,
                                                       Created)
Last sequence
Last annotation
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Last seq
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            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                   C540EF0687F1E998 CRC64;
                                                         annotation
                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Huynh H.T.;
Novel 20.4kD
                                                                                                      293
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                                                       on update)
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                                                                                                                                                                                                                                                                                                    23;
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                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                   272
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                                                                                                                                                                                                            140
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RESULT 7

Q99944

ID Q9994

O1 Q999

D7 01-W
D7 01-D
D8 WGG
OC Euk.
OC Mam
OX NCB
RN [1]
RP SEC
RA RO
RA Bai
RT 10.
RB EK
RT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 28.9%; Score 435.5; Best Local Similarity 37.3%; Pred. No. 3.1 Matches 112; Conservative 36; Mismatcher
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF_like.
Pfam; PF00008; EGF_2.
SMART; SM00179; EGF_CA; 1.
                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; U89336; AAB47494.1; -. HSSP; P3555; 1EMN. Genew; HGNC:13944; C6Orf8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO00152; Asx_hydroxyl.
InterPro; IPRO01881; EGF_Ca.
InterPro; IPRO0189; EGF_like.
Pfam; PF00008; EGF; 2.
SMART; SM00179; EGF CA; 1.
PROSITE; PS001010; A5X_HYDROXYL; 1.
PROSITE; PS001022; EGF_l; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS01186; EGF_CA; 1.
PROSITE; PS01187; EGF_CA; 1.
HYDothetical protein; EGF-like domain.
SEQUENCE 293 AA; 32066 MW; 8A99A5ECO(
                                                                                                                                                                                                                                      Rowen
                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                 kowen L., Dankers C., Baskin D., Faust J.
Banta A., Spies T., Hood L.;
"Sequence determination of 300 kilobases
locus.";
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    Q99944;
01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1997 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q99944
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SEQUENCE FROM N.A.
Rowen L., Mahairas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rowen L., Mahairas G.,
Loretz C., Schmidt S.,
"Sequence of the mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               229 --WATÓAGAMVRAVLÉMPÉEELRPEQVAELMGRGDŘÍEŠLSDÓVLLLEERLGACACEDNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MRGSQEVLIMWLLVLAVG-GTE-HAYRPGRRVCAVRAHGDPV--SESFVQRVYQPFLTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSLASQA---LEHGLP-DPGSLLVHSFQQL----GRIDSLSEQISFLEEQLGSCSCKKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CVPKGGPPRVAPNPTGV------DSAMKEEVQRLQSRVDLLEEKLQLVLAPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VĊTGPDRCECAPGWGGKHCHVDVDECRASLTLCSHGCLNTLGSFLCSCPHPLVLGLDGRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AĞRRICSTYRTTYRVAWREVRREVP-QTHVVCCQGWKKPH--PGALTCDAİCSKPCLNGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CA--GÓPPE---SPTSASILSVAVREADSEEERÁLRWÉVAELRGRLEKLÉQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qin S., Ahearn M.E., Dankers C., Lasky S.,
Tipton S., Traicoff R., Zackrone K., Hood
major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                          Last sequential Last sequential Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Buteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8A99A5EC000A2C62 CRC64;
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annotation update)
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                                                                                                                                                                                       of
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                                                                                                                                                                                                                      Loretz C.,
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                                                                                                                                                                                 human class
                                                                                                                                                                                                                  Ahearn
                                                                                                                                                                                 III MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51;
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Q8IV30
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Best Local S
Matches 102
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Best Local Sim:
Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
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PROSITE;
PROSITE;
PROSITE;
EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                   195
                                                     188
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Q8IV30 PRELIMINARY;
Q8IV30;
01-MAR-2003 (TrEMBLrel. 23, C
01-MAR-2003 (TrEMBLrel. 23, L
01-MAR-2003 (TrEMBLrel. 23, L
                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (UUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC035574; AAH35574.1; -
SEQUENCE 293 AA; 32261 MW; 6519CA255568FFD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chromosome 6 open reading frame 8.
236 PGSLLVHSFQQL----GRIDSLSEQISFLEEQLGSCSCKKDS
                                                                                                                                                                                                                                                            12 LLVLAVGGTEHAYRPGRRVCAVRAHGDPV--SESFVQRVVQPFLTTCDGHRACSTYRTIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 NPTGV-----DSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQA---LEHGLP-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 GWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVAP
                                   SILSVAVREAEKDERALKQEIHELRGRLERLEQ-----
                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                             GWGGKHCHVDVDECRTSITLCSHHCFNTAGSFTCGCPHDLVLGVDGRTCMEGSPEPPTSA 194
                                                                                                                               GWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVAP 187
                                                                                                                                                                 RVMW-REVRREVQQTHAVĆĆQĞWKKRH---PĞALTĆ-EÁİČAKPĆLINĞĞVÇVRPDQCECAP
                                                                                                                                                                                                  RTAYRRSPGLAPARPRYACCPGWKRTSGLPGA--CGAAICQPPCRNGGSCVQPGRCRCPA 127
                                                                                                                                                                                                                                      LLIPGEGAKGGSLRESQGVCSKQTLVVÞLHYNESYSÓÞVYKÞYLTLCAGRRICSTYRTMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGSLLVHSFQQL----GRIDSLSEQISFLEEQLGSCSCKKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SILSVAVREAEKDERALKQEIHELRGRLERLEQ------WAGQAGAWVRAVLPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GWGGKHCHVDVDECRTSITLCSHHCFNTAGSFTCGCPHDLVLGVDGRTCVEGSPEPPTSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00010; ASK_HYDROXYL; 1.
PS00022; BGF 1; 1.
PS01186; BGF 2; 1.
PS01187; EGF_CA; 1.
domain.
293 AA; 32262 MW; 6519CA254FB23FD0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVMW-REVRREVQQTHAVCCQGWKKRH--PGALTC-EAICAKPCLNGGVCVRPDQCECAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RTAYRRSPGLAPARPRYACCPGMKRTSGLPGA--CGAALCQPPCRNGGSCYQPGRCRCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLIPGEGAKGGSLRESOGVCSKQTLVVPLHYNESYSOPVYKPYLTLCAGRRICSTYRTMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLVLAVGGTEHAYRPGRRVCAVRAHGDPV--SESFVQRVYQPFLTTCDGHRACSTYRTIY
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                           ----dsamkeevqrlqsrvdlleeklqlvlaplhslasqa---lehglp-d
                                                                                                                                                                                                                                                                                                                                  27.9%; Score 420.5; DB 4 36.2%; Pred. No. 7.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28.1%; Score 423.5;
36.5%; Pred. No. 4.2
                                                                                                                                                                                                                                                                                                                     38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293
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4.2e-30;
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                                                                                                                                                                                                                                                                                                                                                   DB 4;
                                                                                                                                                                                                                                                                                                             107; Indels
                                                                                                                                                                                                                                                                                                                                                 Length
                             --WAGQAGAWVRAVLPVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
                                                                                                                                                                                                                                                                                                                                               . 293;
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                                                                                                                                                                                                                                                                                                         Gaps
                                                             235
                                                                                                                                                                  134
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RA Adams M.D., Celniker S.E., Lif P.W., Hookkins R.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baddwin D.,
RA Ballew R.M., Basu A., Baxendarle J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Schahet W.M., Glasser K.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., J.A. Ketchum W.,
RA Adams M., Katcha M., J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreft A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreft A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshreft A.,
RA Syles B.C., Siden-Kanno J.A., K
                                PROSITE;
PROSITE;
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                                                                                                                                                        FlyBase; FBgn0035539; CG7447.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001881; EGF Ca.
InterPro; IPR006209; EGF like.
Pfam; PF00008; EGF; 2.
SMART; SM00179; EGF CA; 1.
                                                            PROSITE; PS00010; ASX HYDROXYL; PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 2.
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The genome sequence of Drosophila melanogaster.";
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domain
                                PS01187;
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EGF-like
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PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 1.
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                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008; EGF; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001881; EGF_Ca:
InterPro; IPR006209; EGF_liké.
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Yu C., Lewis S.E., Rubin G.M.,
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Gonzalez M.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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E 512 AA;
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PARP-RYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVD
                                                RHICMQQRTVTMPVKRTEVYSRPTWKHVATPCQPPTFSGQKCTRVQVVHEQAYRDVIDHK 304
                                                                                             RRVC-AVRAHGDPV--SESFVQRVYQPFLTTCD----GHRACSTYRTIYRTAYRRSPGLA
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M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
vis S.E., Rubin G.M., Celniker S.,
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brokstein
                                                                                                                                                                                                                                              57770 MW;
                                                                                                                                                                                                                                                                                                                                                                                            CA;
                                                                                                                                                                                                                                                                                                                                                                                                                             EGF_Likė.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57413 MW;
                                                                                                                                                                    18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P., Hong L., Agbayani A., Carlson J., orsett V., Farfan D., Frise E., George
                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 277.5;
Pred. No. 1.1e
40; Mismatches
                                                                                                                                                                  Score 277.5; DB 5
Pred. No. 1.1e-16;
                                                                                                                                                                                                                                           4DD372E4A6FE7627 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FE4782E4A6E121F0
                                                                                                                                              Mismatches
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                                                                                                                                                                                           DB 5;
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                                                                                                                                                113;
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                                                                                                                                              Indels
                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -KKVSTNADDAFEARDLE
                                                                                                                                                                                           512;
                                                                                                                                           37;
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                                                                                                                                         Gaps
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RESULT 12
Q9UFK6
ID Q9UFF
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088281
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Best Local S
Matches 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UFK6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00010; ASX HYDROXYL;
PROSITE; PS00022; EGF 1; 23.
PROSITE; PS01186; EGF 2; 23.
PROSITE; PS01187; EGF CA; 5.
EGF-11ke domain.
SEQUENCE 1574 AA; 165445 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00008; EGF;
PRINTS; PR00011; EGF
SMART; SM00179; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley; TISSUE-Brain; MEDLINE=98360089; PubMed=9693030; Nadayama M., Nakajima D., Nagase T., Nomura N., Se "Identification of high-molecular-weight proteins like motifs by motif-trap screening."; Genomics 51:27-34(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                             64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; PR00011; EGFLAMI
SM00179; EGF_CA;
                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                           GDGKTCQ-DVDECRAHNGGCQHRCVNTPGSYLCECKPGFRLHTDGRTCL
                                                                                                                                                                                                                                       RPRYACCPGWKRTSGLPGA-----CGAAI--CQPPCRN--GGSCVQPGRCRCPAGWR--
                                                                                                                                                                                                                                                                                                                                 VCAVR-----AHGDPVSESFVQRVYQPFLTTCDGHRAC--STYRTIYRTAYRRSPGLAPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               domain.
1574 AA; 165445 MW;
                                                                                                                                          --GDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCV 177
                                                                                                                                                                                                RTVFRCCPGWSQKPGQEGCLSDVDECASANGGCEGPCCNTVGGF-----YCRCPPGYQLQ
                                                                                                                                                                                                                                                                                      VCAEQKLTLVGHRQPCVQAFSRIVPVWRRTGCAQQAWCIGQERRTVYYMSYRQVYA-TEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLOTNLYKTESRTNKLEGMLNLL
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                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGFLAMININ.
                                                                                                                                                                                                                                                                                                                                                                                                      17.0%;
37.9%;
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08,
23,
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                   Score 256; DB 11;
Pred. No. 3.3e-14;
6; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ம
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2B48533D8F77F6E7 CRC64;
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  558
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1574;
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , Ohara O.;
''tiple EGF-
                                                                                                             204
                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                   156
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RESULT 13
Q9NZL7
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Ford J.E.;

"Cloning of a novel epidermal gr
"EGFL6: expressed in tumor and fe
Genomics 62:304-307(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 57
                                                                                                                                                                                  Q9NZL7
Q9NZL7;
Q9NZL7;
01-OCT-2000
01-OCT-2000
01-MAR-2003
                                                               SEQUENCE FROM N.A.
MEDLINE=20079166; PubMed=10610727;
Yeung G., Mulero J.J., Berntsen R.
                                                                                                              NCBI_TaxID=9606;
                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                              Epidermal growth EGFL6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9UFK6;
01-MAY-2000 (T)
01-MAY-2000 (T)
01-MAR-2003 (T)
Hypothetical pi
DKFZP564P2063.
                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00008; EGF; 4.

pfam; PF00029; MAM; 1.

SMART; SM00179; EGF CA; 3.

PROSITE; PS00010; ASX HYDROXYL; 3.

PROSITE; PS00022; EGF 1; 1.

PROSITE; BS01186; EGF 2; 2.

PROSITE; PS01187; EGF CA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AL117610; CAB56014.1; -.
HSSP; P00736; IAPQ.
Genew: HTMC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Duesterhoeft A., Lauber J., Mewes H.W., Gassenhuber J., Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           139
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                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
57; Conserv
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                                                                                                                                                                                                                                                                                                                                                       VQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCV
                                                                                                                                                                                                                                                                                       YSRTCAMINCOYSCEDTEEGPOCLCPSSGLRLAPN
                                                                                                                                                                                                                                                                                                                                    VGPNKCRCLPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGHMLMPDAT-CV
                                                                                                                                                                                                                                                                                                                                                                                GNAASARHHGLLASA--ROPGVCHYGTKLACCYGWRRNS--KGVC-EATCEPGCK-FGEC
                                                                                                                                                                                   (TrEMBLrel.) (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             558 AA;
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                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                         factor
                                                                                                                                                                                                                                                                                                                ----PKGGPP----
                                                                                                                          Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61828 MW; AA38D7DCE402BFA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                           16.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Fragment).
                                                                                                                                                                   15, Created)15, Last sequence update)23, Last amotation update)repeat containing protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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Last
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 252.5; DB 4
Pred. No. 2.1e-14;
7; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                               growth factor fetal tissues
                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                PRT;
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Catarrhini; Hominidae;
                                                                  .<sub>d</sub>.
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                                 repeat containing .";
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RESULT 14
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                                                                                                                                                                                              Strausberg R.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC038587; AAH38597.1; -.
SEQUENCE 553 AA; 61317 MW; 3AE93A0362E861E0 CRC64;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Similar to EGF-like-domain,
                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2003 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
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PROSITE; PS00022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF CA; 3.
PROSITE; PS0060; MAM 2; 1.
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Pfam; PF00629; MAM;
SMART; SM00179; EGF
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR000998; MAM_domain.
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57; Conserv
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NSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPN
                                               VGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGHMLMPDAT-CV
                                                                                                                     GHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSC
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36.8%;
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36.8%; Pred. No. 2.6e-14;
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                        PKGGPP---
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Pred. No. 2.6e-14;
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RESULT 15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
SEQUENCE 5
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Pfam; PF00629; MAM; 1.
SMART; SM00179; EGF_CA;
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MEDLINE=20241927; PubMed=10777661;
Buchner G., Orfanelli U., Quaderi N., Bassi M.?
"Identification of a new EGF-repeat-containing
Acandidate for developmental disorders.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01186;
PROSITE; PS01187;
PROSITE; PS50060;
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PROSITE; PS00022;
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InterPro;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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IPR001881; EGF_Ca.
IPR006209; EGF_like.
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554 AA; 6
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ilarity 36.8%;
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2; EGF_1; 1.
6; EGF_2; 2.
7; EGF_CA; 3.
7; EGF_CA; 3.
10; MAM_2; 1.
10; MAM_2; M
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Pred. No. 2.6e-14;
7; Mismatches 50
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Result.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
        DB
NTC4 MOUSE
NTC4 HUMAN
NELL2 MOUSE
NELL2 HUMAN
NELL2 RAT
NELL GHICK
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NTC3 HUMAN
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NTC9 HUMAN
NTC9 HUMAN
NTC1 MOUSE
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NTC1 HUMAN
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NTC1 HUMAN
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FRTC PIG
PRTS RAT
FRTC PIG
PRTS RABIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    099435 homo sapien
092832 homo sapien
062918 rattus norv
062919 rattus sall
193555 homo sapien
09um47 homo sapien
09nmy3 homo sapien
09npy3 homo sapien
197207 drosophila
1914543 homo sapien
061554 mus musculu
     Q9r172
Q9g1p2
P98118
                                                                                    P53813
Q9Y219
Q9YE5
P97607
P14585
P21783
P46531
O89103
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Q01705 mus musculu
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Q99466 homo sapien
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                                                                              9 homo sapien
5 mus musculu
7 rattus norv
5 caenorhabdi
3 xenopus lae
1 homo sapien
3 mus musculu
                                                                                                                                                                                                                                                                                  6 homo sapien
2 mus musculu
1 drosophila
3 rattus norv
                                                                                                                                                                                                                                                                                                                                                                                           bos taurus
sus scrofa
mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 homo sapien
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45	44	43	42	41	40	39	38	37	36	35	34
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1213	676	379	456	407	643	2437	2531	618	675	870	833
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JAG3_BRARE	PRTS HUMAN	WIF1 MOUSE	PRTC BOVIN	FA7_BOVIN	CD93_RAT	NTC1_BRARE	NTC1_RAT	DLL3_HUMAN	PRTS_BOVIN	SRC2 HUMAN	SRC2_MOUSE
Q90y54 brachydanio	P07225 homo sapien	Q9wual mus musculu	P00745 bos taurus	P22457 bos taurus	Q9et61 rattus norv	P46530 brachydanio	Q07008 rattus norv	Q9nyj7 homo sapien	P07224 bos taurus	Q96gp6 homo sapien	P59222 mus musculu

ALIGNMENTS

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"Vascular patterning defects associated with expression of activated

SEQUENCE OF VAL-14

Saxena M.T.,

Schroeter E.H.,

Biol. Chem.

Proc.

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entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restitute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mizutani T., Taniguchi Y., Aoki T., Hashimoto I "Conservation of the biochemical mechanisms of among mammalian Notch family members.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POST-TRÂNSLATIUNAL FROCUENT POST-TRÂNSLATIUNAL FROCUENT POST-TRÂNSLATION PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBLEM PROBL
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proteolysis.";
J. Biol. Chem. 276:40268-40273(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Notch4 in embryonic endothelium.";
Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21523956; PubMed=11518718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carcinomas.

SIMILARITY: BELONGS TO THE NOTCH FAMILY.

SIMILARITY: Contains 29 EGF-like domains.

SIMILARITY: Contains 3 Lin/Notch repeats.

SIMILARITY: Contains 5 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: Phosphorylated.

DISEASE: Loss of the extracellular domain causes constitutive activation of the Notch protein, which leads to hyperproliferation of glandular epithelial tissues and development of mammary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytical processing NICD is translocated to the nucleus. TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart kidney, and at lower levels in the ovary and skeletal muscle. A very low expression is seen in the brain, intestine, liver and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity). May regulate branching morphogenesis in the developing vascular system.

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during embryonic development from 9.0 dpc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
FUNCTION: Functions as a receptor for membrane-bound ligands Jagged, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released motth intracellular company is formant transparent to the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released with the released wi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (N
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PRINTS; PRO1452; NOTCH.
SMART; SM00248; ANK; 6.
SMART; SM00179; EGF CA; 11.
SMART; SM00004; NL; 2.
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Pfam; PF00008; EGF; 27.
Pfam; PF00066; notch; 2
PRINTS; PR00010; EGFBLOO
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HSSP; P08709; 1BF9.
MGD; MGI:107471; Not
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; IPR000152; Asx_hydroxyl.

; IPR0000742; EGF_2.

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; IPR001438; EGF_II.

o; IPR006209; EGF_like.

o; IPR002049; LamInin_EGF.
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EGF_CA; 9.
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AAC52630. AAB38377.1; -.

; U43691; AAC52631.1; ; AF030001; AAB82004.1; ; AB016771; BAA32281.1; ; AB016772; BAA32283.1; ; AB016773; BAA32284.1; ; AB016774; BAA32285.1;

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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                              MEDLINE=99180765; PubMed=10079256;
Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
"Human ligands of the Notch receptor.";
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"Human notch4 gene
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MEDLINE=97311416; PubMed=9168133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99466; 000306; Q99458; Q99940; Q9H3S8; 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WEDLINE=97311416; FUDMEGETIOLIC;
Sugaya K., Sasanuma S.-I., Nohata J., Kimura T., Fukagawa T
Sugaya K., Sasanuma S.-I., Noho H., Ikemura T., Mita K.;
Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;
"Gene organization of human NOTCH4 and (CTG)n polymorphism
"Gene organization of mouse proto-oncogene Int3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                      IDENTIFICATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (hNotch4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EQUENCE FROM N.A.
                                                                                                                            J. Pathol. 154:785-794(1999).

FUNCTION: Functions as a receptor for membrane-bound ligands Jaggedl. Jaggeda and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with
            RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May regulate branching morphogenesis in the developing vascular system (By similarity).

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the human NOTCH4 gene."; 51:45-58(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                     OF 1-503 FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RDINECFLEPGPCPQGTSCHNTLGSYQCLCPVGQEGPQCKLRKGACPPGSCLNGGTCQLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDVDECSARRGGCPQ--RCINTAGSYWCQC---WEGHSLSADGTLCVP----KGGPPRVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ASGRPQCSCEPGWTGEQCQLRDFCSA----NPCANGGVCLATYPQIQCRCPPGFEGHTCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PNP-----TGVDSAMKEE 199
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                                                                                                                                                                                                                                                                                                                                                           (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                              Tokunaga K., Hojho H.;
4 gene variant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human)
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                                                                                                                                                                                                                                                                                                                      LIGANDS
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Pred. No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                     AND VARIANTS GLN-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y., Smith T., Dong P., pies T., Rowen L., Hood L.; complete 56.8-kilobase DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POLYMORPHISM OF
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Q9UII9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               precursor (Notch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1964;
                                                                                                                                                                                                                                                                                                                                                                                                                     AND GLN-317.
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InterPro; IPR002110; ANK.
InterPro; IPR000152; Asx hydroxyl.
InterPro; IPR000162; EGF-2.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001438; EGF_II.
InterPro; IPR006209; EGF-like.
InterPro; IPR0062049; Laminin_EGF.
InterPro; IPR000800; Notch.

EMBL; AB023961; BAB20317.1; -.
EMBL; AB024520; BAA68951.1; -.
EMBL; AB024578; BAA68952.1; -.
HSSP; P08709; 1BF9.

Genew; HGNC: 7884; NOTCH4.

PRINTS;

PR00011;

EGFBLOOD. EGFLAMININ.

; PR01452; SM00248; A

, NOTCH ANK; 5 EGF_CA; 11.

Pfam; PF00023; ank; 6.
Pfam; PF00008; EGF; 26.
Pfam; PF00066; notch; 2
PRINTS; PR00010; EGFBLO

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EMBL; D86566; BAA13116.1; --
EMBL; U95299; AAC32288.1; --
EMBL; U9335; AAC63097.1; --
EMBL; AB023361; BAB20317.1;
                                                                            EMBL; D63395; BAA09708.1; ALT_FRAME
                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteolytical processing NICD is translocated ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                        in position 1438 to 1463.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral blood leukocytes.
PTM: Synthesized in the endoplasmic reticulum as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=Q99466-3; Sequence=VSP_001407; TISSUB_SPECIFICITY: Highly expressed in the heart, moderately in the lung and placenta and at low levels in the liver, skeletal muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow and fetal liver. No expression was seen in adult brain or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: Type I membrane protein. Following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q99466-1;
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                                                                                                                                                                                                                              EMBL
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PROSITE; PSS0086; ANK REPEAT; 5.

PROSITE; PSS0097; ANK REP REGION; 1.

PROSITE; PS00010; ASX HYDROXYL; 11.

PROSITE; PS00010; EGF 1; 28.

PROSITE; PS001187; EGF CA; 9.

PROSITE; PS01187; EGF CA; 9.

Receptor; Transcription regulation; Act Developmental protein; Repeat; ANK reprosers of the proportion of the property of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the process of the p
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Beckmann G., Hanke J., Bork P., Reich J.;
"Merging extracellular domains: fold prediction
and amino-terminal thrombospondin-like modules b
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InterPro; IPR00
Pfam; PF00008;
Pfam; PF02210;

EGF;

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Pfam; Pfam;

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SMART; SMO214; VWC; 2.

PROSITE; PS00010; ASX HYDROXYL; 3.

PROSITE; PS00102; EGF 1; 1.

PROSITE; PS01187; EGF CA; 3.

PROSITE; PS01187; WFC 1; 2.

PROSITE; PS01208; VWFC 2; 2.

PROSITE; PS0184; VWFC 2; 2.

Glycoprotein; EGF-1ike domain; Repsignal 1
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SMART; SM00179; EgF CA; 3.
SMART; SM00210; LamG; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 2.
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47; Conserv
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29.4%;
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POTENTIAL.

PROTEIN KINASE C-BINDING PI
TSP N-TERWINAL.

VWFC 1.

VWFC 2.

EGF-LIKE 2, CALCIUM-BINDING
EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 5, CALCIUM-BINDING
EGF-LIKE 5, CALCIUM-BINDING
EGF-LIKE 5, CALCIUM-BINDING
EGF-LIKE 6, CALCIUM-BINDING
UWFC 3.

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                                                                                                                                                                                                                                                                                                                                                                                                              64;
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       NRGI, 95490, Fbin2.

NRGI, 960, 0030326; P:limb morphogenesis; IMP.

RINCETPRO; IPR000152; Asx hydroxyl.

RINCETPRO; IPR001831; EGF_CI.

NR INTERPRO; IPR001831; EGF_II.

RINCETPRO; IPR002209; EGF_II.

RINCETPRO; IPR002212; Fibril-assoc.

Pfam; PF00008; EGF; 45.

NR PF100008; EGF; 45.

NR PF100008; EGF; 45.

NR PRNST; PR00010; EGFELOOD.

NR PRNST; PR00010; EGFELOOD.

NR PRNST; PR00010; EGF CA; 43.

NR PROSITE; PS00106; ASX HYDROXYL; 43.

NR PROSITE; PS00102; EGF_1; 2.

NR PROSITE; PS01186; EGF_2; 36.

NR PROSITE; PS01186; EGF_2; 36.

NR PROSITE; PS01187; EGF_CA; 43.

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15-DEC-1998 (Rel.
15-DEC-1998 (Rel.
28-FEB-2003 (Rel.
Fibrillin 2 precur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Fibrillin genes map to regions of conserved mouse/human synteny on mouse chromosomes 2 and 18.";

Genomics 18:667-672(1993)
-i- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILIN-1-CONTAINING MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
-i- SIMILARITY: Contains 47 EGF-like domains.
-i- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
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                                                                                                                                                                                                                                                                                       Repeat;
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fibrillin 2 precursor.
FBN2 OR FBN-2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L39790; AAA74908.1; -. EMBL; S69359; AAC60685.1; -. EMBL; A57278; A57278.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Cell Biol. 129:1165-1176(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhang H., Hu W., Ramirez F.; "Developmental expression of fibrillin of extracellular microfibrils.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 210-317 FROM N.A. MEDLINE=94140368; PubMed=8307578;
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[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95263670;
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                                                                                                                                                                                                                                                                                                             Signal;
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FIBRILLIN
EGF-LIKE 1
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TGFBP. 1.
EGF-LIKE 7
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EGF-LIKE 9
EGF-LIKE 9
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RESULT 5
NEL2_HUMAN
      GG; GO:0005576; C:extracellular; NAS.
GG; GO:0005509; F:calcium ion binding ac
GG; GO:0005198; F:structural molecule ac
GG; GO:0005198; F:sell adhesion; NAS.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR00152; Asx.hydroxyl.
InterPro; IPR006209; EGF like.
InterPro; IPR001791; LamInin_G.
InterPro; IPR001791; LamInin_G.
InterPro; IPR001791; LamInin_G.
InterPro; IPR001791; VWF_C.
pfam; PF00008; EGF; 5.
pfam; PF00008; EGF; 5.
pfam; PF00009; VWc; 3.
pfam; PF00093; VWc; 3.
pfam; SM00210; TSPN; 1.
sMART; SM00210; TSPN; 3.
sMART; SM00210; TSPN; 3.
sMART; SM00210; TSPN; 3.
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GO; GO:000
GO; GO:000
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InterPro;
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                               Genew; HGNC:7751; NELL2.
MIM; 602320; -.
                                                                                                                                                                                                                                                                                           EMBL; D83018;
HSSP; P00740;
                                                                                                                                                                                                                                                                                                                                     or, send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                     modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pentraxins.";
J. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98153258; PubMed=9480764;
Beckmann G., Hanke J., Bork P., Reich J.;
"Merging extracellular domains: fold prediction for laminin G-like
and amino-terminal thrombospondin-like modules based on homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein kinase C-binding (Nel-related protein 2).
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MEDLINE=97131504; PubMed=8975702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOI. Biol. 275:725-730(1998).
SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
SUBCELLULAR LOCATION: Secreted (By similarity).
SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
SIMILARITY: Contains 5 VWFC domains.
SIMILARITY: Contains 6 EGF-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-TERMINAL
                                                                                                                                                                                                                                                                                                                                                                                              European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T., bto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.; ling and characterization of two novel human cDNAs (NELL1 and encoding proteins with six EGF-like repeats."; lcs 38:273-276(1996).
                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long as its content is in and this statement is not removed. Usage by and for correquires a license
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Primates;
                                                                                                                                                                                                                                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce/
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Catarrhini; Hominidae;
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e activity;
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) NEL1 HUMAN STANDARD; PRT; 810 AA.
) Q92832; Q9Y472;

f 01-NOV-1997 (Rel. 35, Created)

f 16-OCT-2001 (Rel. 40, Last sequence update)

f 28-FEB-2003 (Rel. 41, Last annotation update)

E Protein kinase C-binding protein NELL1 precuric (Nel-related protein 1).
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Best Local
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Glycoprot
SIGNAL
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGG 147
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; EGF_2; 4.
; EGF_CA; 3.
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; VWFC_2; 3.
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: EGF-LIKE 2, CALCIUM-
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5, CALCIUM-
EGF-LIKE 6, CALCIUM-
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EGF-LIKE 5, CALCIUM-

EGF-LIKE 3.

EGF-LIKE 5, CALCIUM-

EGF-LIKE 3.

EGF-LIKE 3
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Pred. No. 8.5e
3; Mismatches
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PROTEIN KINASE C-BINDING
TSP N-TERMINAL.
  Craniata; Ve
Catarrhini;
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                             Vertebrata;
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     Hominidae;
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, GO:0007399; P:In...
, GO:0007399; P:In...
, GO:0007399; P:In...
, GO:0007399; P:In...
, IPRO001881; EgF_Ca.

InterPro; IPR000189; EgF_like.
InterPro; IPR001791; LamInin.G.
InterPro; IPR00179; VWF_C.
, IPR00179; TSPN.
InterPro; IPR00107; VWF_C.
, Pfam; PF002008; EgF; 5.

Pfam; PF002010; TSPN; 1.
DR Pfam; PF0020179; EgF_CA; 2.
SMART; SM00219; TSPN; 1.
SMART; SM00210; TSPN; 1.
SMART; SM00214; VWC; 3.
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                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D83017; BAA11680.1; -.
EMBL; U57523; AAB06946.1; ALT_FRAME
HSSP; P07204; 1ADX.
Genew, HGNC:7750; NELL1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E. "Cloning and characterization of two novel human cDNAs (NELL NELL2) encoding proteins with six EGF-like repeats."; Genomics 38:273-276(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606; [1]
                                                                                                                                            Glycoprotein;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vastardis H.,
, Tieu A., Kwo
                                                                                                                                                                                                                                                                                                                                          ; P:neurogenesis; TAS
00152; Asx_hydroxyl.
01881; EGF_Ca.
06209; EGF_like.
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PROTEIN KINASE OF TSP N-TERMINAL.

VMFC 1.

VMFC 2.

EGF-LIKE 1.

EGF-LIKE 2, CALC

EGF-LIKE 3.

EGF-LIKE 4.

EGF-LIKE 6, CALC

EGF-LIKE 6, CALC

VMFC 3.

VMFC 5.
                                                                                                                                                       Repeat; Signal.
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                                                                                                                                 KINASE C-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bertolami C.,
                                CALCIUM-BINDING CALCIUM-BINDING
                                                                           CALCIUM-BINDING
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                                                                                                    SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Brain
MEDLINE-20017976; PubMed-10548494;
                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                    Biochem.
                                                Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizav
Abe T., Matsuhashi S., Ting K.;
"Biochemical characterization and expression analysis
thrombospondin-1-like proteins NELL1 and NELL2.";
                                                                                                                                              NCBI_TaxID=10116;
[1]
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                   Rattus norvegicus (Rat).
                                                                                                                                                                                                              Protein kinase
NELL2 OR NEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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MEDLINE=98153258; PubMed=9480764;
           TSP N-TERMINAL DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                  Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                 CHNHSRCVNLPGWYHCECRSGFHDDGTYSLSGESCI
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Sciurognathi; Muridae;
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InterPro; IPRO0015; Asx_hydroxyl.
InterPro; IPR00181; EGF Ca.
InterPro; IPR001209; EGF Ike.
InterPro; IPR001201; LamInin G.
InterPro; IPR0011791; LamInin G.
InterPro; IPR0011791; VwF C.
Pfam; PF00008; EGF; 5.
Pfam; PF00008; EGF; 5.
Pfam; PF000093; vwc; 3.
SMART; SM00179; EGF CA; 3.
SMART; SM00179; EGF CA; 3.
SMART; SM00101; ASX HYDROXYL; 3.
PROSITE; PS001010; ASX HYDROXYL; 3.
PROSITE; PS01186; EGF Z; 4.
PROSITE; PS01187; EGF CA; 3.
PROSITE; PS01187; EGF CA; 3.
PROSITE; PS01187; EGF CA; 3.
PROSITE; PS01187; EGF Z; 4.
PROSITE; PS01187; EGF Z; 4.
PROSITE; PS01187; EGF Z; 3.
PROSITE; PS01187; EGF Z; 3.
PROSITE; PS01187; EGF Z; 4.
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PROSITE; PS01187; EGF Z; 3.
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J. Mol. Biol. 275:725-730(1998).

-!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN)
-!- SIMILARITY: Contains 5 VWFC domains.
-!- SIMILARITY: Contains 6 EGF-like domains.
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P00740;
      AAC72245.1; -.
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      domain;
in; Repeat; Signal.
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PROTEIN KINASE C-B
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VWFC 2.
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EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5, CALCIU
EGF-LIKE 6, CALCIU
UNFC 3.
EGF-LIKE 6, CALCIU
UNFC 3.
EGF-LIKE 7.
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Matches 35
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"Biochemical characterization and expression analysi thrombospondin-1-like proteins NELL1 and NELL2.";
Biochem. Biophys. Res. Commun. 265:79-86 (1999).
-!- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) dom
-!- SIMILARITY: Contains 5 VWFC domains.
-!- SIMILARITY: Contains 6 EGF-like domains.
InterPro; iPR000152; Asx hydroxyl.
InterPro; iPR00181; EGF Ca.
InterPro; IPR001801; EGF like.
InterPro; IPR001791; Laminin G.
InterPro; IPR001791; Taminin G.
InterPro; IPR001797; VWF C.
Pfam; PF00008; EGF; 5.
Pfam; PF00008; EGF; 5.
SMART; SM00179; EGF CA; 2.
SMART; SM00210; TSPN; 1.
SMART; SM00210; TSPN; 1.
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SEQUENCE
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PIR; T10756; T10756.
HSSP; P35555; 1EMN.
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MEDLINE=20017976; PubM
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein kinase C-binding protein NELLI precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
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PROSITE; PS00010; ASX HYDROXYL; 3
PROSITE; PS00022; EGF 1; 1.

PROSITE; PS01186; EGF 2; 3.

PROSITE; PS01187; BGF CA; 3.

PROSITE; PS01208; VWFC 1; 2.

PROSITE; PS50184; VWFC 2; 2.
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. 35, Created)
. 35, Last sequence upda
. 37, Last annotation up
ursor (93 kDa protein).
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EGF-LIKE 2, CAI
EGF-LIKE 3.
EGF-LIKE 4.
EGF-LIKE 5, CAI
EGF-LIKE 6, CAI
WWFC 3.
VWFC 5.
VWFC 5.
VWFC 5.
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VWFC 5.
EGF-LIKE 6, CAI
UWFC 3.
EGF-LIKE 6, CAI
UWFC 3.
EGF-LIKE 6, CAI
UWFC 3.
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UWFC 3.
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UWFC 3.
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EGF-LIKE 5, CAI
UWFC 3.
EGG-LIKE 5
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Pred. No. 1.3e
13; Mismatches
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POTENTIAL.
PROTEIN KINASE C-BINDING PROTEIN NELL1.
TSP N-TERMINAL.
VWFC 1.
VWFC 2.
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    PÉAM; PF00008; EGF; 5.
PÉAM; PF00003; VWC; 3.
PÉAM; PF000093; VWC; 3.
SWART; SM00179; EGF CA; 2.
SWART; SM00282; LAMG; 1.
SWART; SM00282; LAMG; 1.
SWART; SM00214; VWC; 2.
PROSITE; PS001010; ASX HYDRO;
PROSITE; PS001010; ASX HYDRO;
PROSITE; PS001186; EGF—1; 1.
PROSITE; PS001186; EGF—2; 4.
PROSITE; PS01186; EGF—2; 4.
                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF like.
InterPro; IPR001791; LamInin_G.
InterPro; IPR001791; TSPN.
InterPro; IPR001007; VWF_C.
Pfam; PF00008; EGF; 5.
 Glycoprotein;
SIGNAL
CHAIN 2
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DOWAIN 33
DOWAIN 39
DOWAIN 44
DOWAIN 48
DOWAIN 55
DOWAIN 55
DOWAIN 55
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J. Mol. Biol.
-!- TISSUE SPE
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Dev. Dyn.
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MEDLINE=98153258; PubMed=9480764;

Beckmann G., Hanke J., Bork P., Reich J.;

Beckmann g., Hanke J. Bork P., Reich J.;

"Merging extracellular domains: fold prediction for laminin G-like
"Merging extracellular domains: fold prediction for laminin G-like
and amino-terminal thrombospondin-like modules based on homology to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matsuhashi S., Noji S., Koyama E., Myokai F., Ohuchi H., Taniguchi S., Hori K.; Taniguchi S., nel, encoding a M(r) 93 K protein with EGF-like repeats strongly expressed in neural tissues of early stage chick embryos." Dev. Dyn. 203:212-222(1995).
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Gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D86747; BAA13167.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOI. 275:725-730(1998).

MOI. Biol. 275:725-730(1998).

TISSUES SPECIFICITY: STRONGLY EXPRESSED IN EARLY EMBRYONIC NEURAL TISSUES (BRAIN, SPINAL CORD, DORSAL ROOT GANGLIA); LESS IN OTHER TISSUES SUCH AS CELLS AROUND CARTILAGE, MYOCARDIUM, LUNG MESENCHYMAL CELLS, AND LIVER. AFTER HATCHING EXPRESSION IS RESTRICTED TO NEURAL TISSUES INCLUDING REFINA.

SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.

SIMILARITY: Contains 5 VWFC domains.

SIMILARITY: Contains 6 EGF-like domains.
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25
272
272
272
332
397
4440
4482
5555
5555
                                                                                                                                                          ASX HYDROXYL;

EGF_1; 1.

EGF_2; 4.

EGF_C; 3.

VWFC_1; 2.

VWFC_2; 3.
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ji S., Koyama E., Myokai F., Ohuchi H.,
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816
258
3316
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396
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637
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TSP N-TER
TSP N-TER
VWFC 1.
WWFC 2.
EGF-LIKE
EGF-LIKE
EGF-LIKE
EGF-LIKE
EGF-LIKE
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  CALCIUM-BINDING CALCIUM-BINDING
                                                       CALCIUM-BINDING
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Best Local
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P3555;
01-JUN-1994
01-JUN-1994
28-FEB-2003
Fibrillin 1
                                                                                                                     SEQUENCE TISSUE=Fi
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FBN1 I
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            Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau "Fibrillin binds calcium and is coded by cDNAs that multidomain structure and alternatively spliced exor
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CARBOHYD
                                                                                      SEQUENCE OF 1-932 FROM N.A.
TISSUE=Fibroblast, and Placenta;
MEDLINE=94010947; PubMed=7691719;
                                                                                                                                                                                                                   defective
                                                                                                                                                                                                                                                                 Pereira L.V., D'Alessio
Pangilinan T., Bonadio I
                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=93372860;
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Mammalia; Eutheria;
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e gene product in Marfan syndrome.
. Genet. 2:961-968(1993).
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lessio M., Ramirez
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Primates;
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Pred. No. 2.5e
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Corson G.M., Puffenberger E:G., Hamosh
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                                                                                                                                                                                                                                                                                          Peltonen L.;
wo defective
                                                                                                 ism in EGF-like of exons 15-21
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                                                                                                                                                                                                                                                                                                                                                                                                         Levitt D.,
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                                                                                                                                                                                        ectopia lentis.";
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                         Kristofersson
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domains."
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Cutting
epidermal growth
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the fibrillin
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Marfan syndrome
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                                                                                                    in Marfan
                                                                                                              domains
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RESULT 11

NTC3
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DT 28-FF
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OC Eukan
OC Mamma
OX NCB1
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RN [1]
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RA Joutt
RA Bach
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Best Local
                                                                                                                                                                                                                                  HUMAN
NTC3_F
                                                                                                                                                                            NTC3_HUMAN STANDARD; PRT; 23
Q9UM47; Q9UEB3; Q9UFL3; Q9Y6L8;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kainulainen K., Karttunen L., Puhakka L., Sak "Mutations in the fibrillin gene responsible lentis and neonatal Marfan syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           variant of Marfan
J. Clin. Invest. 9
[22]
             Joutel A., Corpechot C., Ducros A., Vahedi K., Chabrid Alamowitch S., Domenga V., Cecillion M., Marechal E., Vayssiere C., Cruaud C., Cabanis E.-A., Ruchoux M.M., Bach J.-F., Bousser M.-G., Tournier-Lasserve E.;
                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arachnodactyly
                                                                SEQUENCE FROM N.A. MEDLINE=97032728;
                                                                             SEQUENCE
                                                                                                                                           Homo sapiens
                                                                                                                                                        Neurogenic
NOTCH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94184368;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "A novel mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayward C., Porteous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95174777;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               factor-like motifs of the FBN1 polypeptide is connected to a novel
                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS MFS GLY-217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genet.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cell. Probes 8:325-327(1994).
                                                                                                                                                                                                                                                                                                 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
59; Conserv
  mutations
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                                                                                                                                                                                                                                                                                                  NTVSSYFCKCPPGFYTSPDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGGNQCIVFICRHSCGDGFCSR---PNMCTCPSGQIAPSCGS-RSIQHCNIRCMNGGSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR---ACSTYRTIYRTAYRRSPGLAPA
                                                                                                                                                                                                                                                                                                                                                   DVDECQAIPGLCQGGNCINTVGSFECKCPAGHKLNEVSQKCEDIDECSTIPGICEGGECT
                                                                                                                                                                                                                                                                                                                                                                         DVDECSARRGGCP-QRCINTAGSYWCQCWEGHSLSADGTLC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDHCLCQKGYIGTH----
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                                                                                                                                                                     locus notch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6:64-69(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1682; PubMed=8071963;
Lynch J.R., Child A., Sykes
nse mutation of fibrillin in
                                                                                                                                           (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 syndrome.";
94:709-713(1994)
  ij
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ous M.E.M., Brock
in the fibrillin
                                                                 PubMed=8878478;
                                                                                                                                                                                                                                                                                                                          PPRVAPNETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; ASN-1023; F
LYS-2447 AND
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  CADASIL,
                                                                                                                                                                   homolog protein
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Pred. No. 9.1e-06;
                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                         191
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  hereditary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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patient
  adult-onset
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                         Chabriat H., Mouton hal E., Maciazek J. x M.M., Weissenbach
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                                                                                                                                                                                                                                                                                                                                                     305
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dementia.";

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Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L., Banks A., Leiman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas "Human ligands of the Notch receptor.";
Am. J. Pathol. 154,785-794 (1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VARIANT CADASIL 114-GLY--PRO-120 DEL.
VARIANT CADASIL 114-GLY--PRO-120 DEL.
WARIANT CADASIL 114-GLY--PRO-120 DEL.
WEDLINE-20264473; PubMed=1808207;
Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,
Joutel A., Chabriat H., Vahedi K., Domenga V., Vayssiere C.,
Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserve
Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserve
Ruchoux M.M., Lucas C., Leys D., Bousser M.-G., Tournier-Lasserve
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Nature 3
[2]
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[6]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Strong clustering and stereotyped nature CADASIL patients.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-13; CYS-14AG; CYS-146; CYS-153; CYS-169; CYS-171; CYS-122; ARG-185; SER-212; GLY-222; TYR-224; CYS-258; TYR-542; CYS-558; CYS-578; CYS-728; CYS-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.

MEDLINE=98049753; PubMed=9388399;
Joutel A., Vahedi K., Corpechot C., Troesch A., Chabriat H., Vaysstere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-Bach J.-F., Tournier-Lasserve E.;
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          PTW: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-Golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(EC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NET). This fragment is then cleaved by presentiln dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                    bonds (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein.
proteolytical processing NICD is translocated to TISSUE SPECIFICITY: Ubiquitously expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Deltal to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NTCD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity).

SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(EC) which are probably linked by disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Artavanis-Tsakonas
(APR-1998) to the J
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Pfam; PF00023; ank; 6.
Pfam; PF00008; EGF; 34.
Pfam; PF000066; notch; 3.
Pfint; PF000066; notch; 3.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00011; NOTCH.
SMART; SM00248; NOTCH.
SMART; SM00143; NUTCH.
SMART; SM00179; EGF_CA; 19.
SMART; SM00179; EGF_CA; 19.
SMART; SM00179; EGF_CA; 19.
SMART; SM00179; ANK_REPEAT; PROSITE; PS50089; ANK_REPREGIPROSITE; PS00010; ASX_HYDROXYIPPROSITE; PS00010; ASX_HYDROXYIPPROSITE; PS0001187; EGF_CA; 33.
PROSITE; PS001187; EGF_CA; 16.
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SIMILARITY: BELONGS TO THE NOTCH FAMILY.
SIMILARITY: Contains 34. EGF-like domains.
SIMILARITY: Contains 3 Lin/Notch repeats.
SIMILARITY: Contains 5 ANK repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          autosomal dominant arterion leukoencephalopathy) which which key features include
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DISEASE: Defects in NOTCH3 are associated with CADASIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | IPR002110; ANK.
| IPR002112; Asx hydroxyl.
| IPR000142; EGF_2.
| IPR001891; EGF_Ca.
| IPR001438; EGF_II.
| IPR006209; EGF_IIke.
| IPR002049; Laminin EGF.
| IPR002049; Laminin EGF.
             Transcription regulation; Activator; Differentiation; ntal protein; Repeat; ANK repeat; EGF-like domain; rane; Glycoprotein; Signal; Phosphorylation; Polymorph
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                                                                                             ; ANK REPEAT; 4.
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; ASX HYDRAM;
; EGF 1; JR
; EGF 2; 25.
; EGF CA; 16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions on it ng as its content is in roved. Usano t
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Knapp Selenko Knapp W.;

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AC __Q9NPi
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DT __15-G
DE __COMp
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Complement component Clq receptor precursor (Complement component 1, subcomponent, receptor 1) (ClqRp) (ClqR(p)) (Clq/MBL/SPA receptor)
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%;
     structure analysis
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CYTOPLASMIC
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
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EGF-LIKE 7.
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EGF-LIKE 25.
EGF-LIKE 25.
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Pred. No. 8.8e-06;
4; Mismatches 44
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NOTCH INTRACELLULAR
SIMILARITY).
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NEUROGENIC LOCUS NOTCH HOMOLOG NOTCH EXTRACELLULAR TRUNCATION
                                                                                                                                                                  Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                               Burgess
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                                                                                                                                                                     Hominidae;
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s W.H., Tenner A. of ClqR(P), the
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M-BINDING
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     human
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     REPRESENTATION OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
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RX MEDLINE=22388257 pubMed=12477932;
RX MEDLINE=22388257 pubMed=12477932;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RX Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
RA Aleschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Raha S., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butkersley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Butkersley A.C., Grimwood J., Schmutz J., Myers R.M.,
"Generation and initial ahalysis of more than 15,000 full-length
"In human and mouse cDNA sequences.",
"Froc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., RA Deloukas P., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., RA Bailey J., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Eird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., RA Beasley O.P., Clarmp M., Clark G.Y., Clark K.N., Clark S.Y., Clee C.M., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., RA Huntkle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Lavlor S. RA Hammond S., Harley J.L., McConnachie L.J., McLay K., McMurray A.A., RA Milne S.A., Matry D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Diversiaho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Kowntray A.A., RA Milne S.A., Natery D., Moore M.J.F., Mullikin J.C., Nickerson T., RA Phillimns S.A., Patel R., Pearce T.A.V., Peck A.I., RA Phillimns S.A., Sycamore N., Taylor R., Sehra H.K., Shownkeen R., Sims S., Sawann R.M., Sycamore N., Taylor R., Sehra H.K., Shownkeen R., Sims S., Sawann R.M., Sycamore N., Taylor R., Wallis J.M., Thorpe A., RA Willehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., RA Willehead S.L., Whittaker P., Willey D.L., Williams S.A., Beck S., RA Roders J., Wallis J.M., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
  O-GLYCOSYLATION
                                                                                                                                CHARACTERIZATION.
MEDLINE=21990337; Publ
McGreal E.P., Ikewaki
                                                                               "Human ClqRp is
not bind Clq.";
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Steinberger P., Szekeres A.; Wille S., Stockl J.,
Prager E., Staffler G., Madic O., Stockinger H., 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clq/MBL/SPA receptor that mediates enhanced phagocytosis in vitro."; Immunity 6:119-129(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NA sequence and comparative analysis of human 414:865-871(2001).
                                                                                                                             .P.,
                                                        168:5222-5232 (2002)
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identical
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                                                                                                                                     PubMed=11994479;
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                                                                                                               Akatsu H. with CD93
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chromosome 20.";

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B.P., Gasque P. mNI-11 antigen

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GO; GO:0042116; P:macrophage activation; NAS.
GO; GO:0006909; P:phagocytosis; NAS.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR0010304; Lectin_C: 1.
Pfam; PF00008; EGF; S.
Pfam; PF00108; Tissue_fac; 1.
Pfam; PF00108; Tissue_fac; 1.
SMART; SM00134; CLECT; 1.
SMART; SM00134; CLECT; 1.
SMART; SM00179; EGF_CA; 3.
PROSITE; PS00010; ASX_HYDROXYL; 3.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
PROSITE; PS001186; EGF_C; 3.
PROSITE; PS01186; EGF_C; 3.
PROSITE; PS01186; EGF_C; 3.
PROSITE; PS01186; EGF_C; 3.
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J. Immunol.
-!- FUNCTION
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DOMAIN
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EMBL; BC028075; AAH28075.1;
HSSP; P35555; 1EMN.
Genew; HGNC:15855; C1QR1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein.

I SUBCELLULAR LOCATION: Type I membrane protein.

I TISSUE SPECIFICITY: Highly expressed in endothelial cells, platelets, cells of myeloid origin, such as monocytes and neutrophils. Not expressed in cells of lymphoid origin.

I PTM: N- and O-glycosylated.

I SIMILARITY: Contains 1 C-type lectin family domain.

SIMILARITY: Contains 5 EGF-like domains as collectin receptor.

CAUTION: Has been sometimes referred to as a collectin receptor.

CAUTION: According to Ref. 5, Clq is not a ligand for ClQR1.

DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);

WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456_g.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U94333; AAB53110.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0016021; C:integral to membrane; GO:0004872; F:receptor activity; NAS GO:0016337; P:cell-cell adhesion; ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: Receptor (or element of a larger receptor complex) Clq, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis monocytes and macrophages upon interaction with soluble defen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulation of
                                                                                                                                                                                                                                                                                                          domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ion of phagocytic activity."; 162:3583-3589(1999).
                                                                                                                                                                                                                                                                                                      Receptor; Repeat; Signal; Transmembrane; n; Lectin; Glycoprotein; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=10092817;
EGF-LIKE 2.
EGF-LIKE 3. CALCIUM-BINDING (
EGF-LIKE 4. CALCIUM-BINDING (
EGF-LIKE 5. CALCIUM-BINDING (
EGF-LIKE 2. CALCIUM-BINDING (
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                                                                                                                                                                    POTENTIAL.
CYTOPLASMIC (PC
C-TYPE LECTIN.
EGF-LIKE 1.
                                                                                                                                                                                                                                                 COMPLEMENT COMPONENT C1Q RECEPTOR. EXTRACELLULAR (POTENTIAL).
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P07207; O97458; P04154; Q9W4T8; O1-NOV-1986 (Rel. 03, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neurogenic locus Notch protein precursor.
N OR EG:140G11.1 OR EG:163A10.2 OR CG3936.
                                                                                                                                                                               Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                         Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas "Nucleotide sequence from the neurogenic locus notch i product that shares homology with proteins containing
           SEQUENCE FROM N.A.
STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo:
                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Oregon-R; TISSUE-Embryo;
MEDLINE=87064624; PubMed=3097517
                                                                                                                 MEDLINE=86079539; PubMed=3935325;
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                                                 43:567-581 (1985)
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Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
Benos P.V., Gatt M.K., Ashburner M., Murphy L., Demailes J., Cadieu E
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailes J., Cadieu E
Barrell B.G., Ferraz C., Vidal S., Brun C., Demailes J., Cadieu E
Dreano S., Gloux S., Lelaure V., Mottier S., Gallbert F., Borkova
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
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                                                                           and other developmentally regulated Cell 40:55-62(1985).
                                                                                                                                                                                     MEDLINE=85099329; PubMed=2981631; Wharton K.A., Yedvobnick B., Finnerty V.G., "opa: a novel family of transcribed repeats
                                                                                                                                                                                                                                                                                                                                                                           melanogaster.";
Science 287:2220-2222(2000)
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MEDLINE=87257846;
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R GO; GO:0005634; C:nucleus; NAS.
R GO; GO:0005886; C:plasma membrane; IDA.
GO; GO:0004888; F:transmembrane receptor activity; NAS.
R GO; GO:0004888; F:transmembrane receptor activity; NAS.
R GO; GO:0007403; P:determination of glial fate; IMP.
R GO; GO:0007293; P:egg chamber formation; IMP.
R GO; GO:0042067; P:estrablishment of ommatidial polarity (se
GO:00046331; P:lateral inhibition; NAS.
R GO; GO:0007498; P:mesoderm development; IMP.
R GO; GO:0007498; P:myogenesis; IMP.
R GO; GO:0007519; P:myogenesis; IMP.
R GO; GO:00045465; P:R8 differentiation; NAS.
R GO; GO:00045465; P:R8 differentiation; NAS.
R GO; GO:00045465; P:R8 differentiation; NAS.
R GO; GO:0007423; P:regulation of R8 spacing; NAS.
R GO; GO:0007424; P:tracheal system development (sensu Insec
R GO; GO:0007476; P:wing morphogenesis; NAS.
R GO; GO:0007476; P:wing morphogenesis; NAS.
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EMBL; M16149; AAB59220.1; JOINED.
EMBL; M16149; AAB59220.1; JOINED.
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EMBL; M16151; AAB59220.1; JOINED.
EMBL; K03508; AAA28725.1; JOINED.
EMBL; K03508; AAA28725.1; JOINED.
EMBL; K03507; AAA28725.1; JOINED.
EMBL; K03507; AAA28725.1; JOINED.
EMBL; K03507; AAA28725.1; JOINED.
EMBL; K03505; CAB37610.1; -.
EMBL; AL035436; CAB37610.1; -.
EMBL; AL035436; CAB37610.1; -.
EMBL; M1025436; CAB37610.1; -.
EMBL; M1025436; CAB37610.1; -.
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"Many cell types specified by Notch function.";
Curr. Biol. 1:120-122(1991).
                                                                                                                                                                                                        InterPro;
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"Restriction
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Pro; IPR002110; ANK.

Pro; IPR000152; Asx hydroxyl.

Pro; IPR000742; EGF_2.

Pro; IPR000742; EGF_1.

PRO; IPR001488; EGF_11.

PRO; IPR006209; EGF_1ike.

PRO; IPR002049; Laminin_EGF.
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                                              PF00023; ank; 7
PF00008; EGF; 3
PF00066; notch;
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IPR000800;
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P14543; Q14942;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last seq
15-SEP-2003 (Rel. 42, Last and
                                                                      SEQUENCE FROM N.A.
MEDLINE=90091745; PubMed=2574658;
Magayoshi T., Sanborn D., Hickok
Chu M.-L., Knowlton R., Mann K.,
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Mammalia; Eutheria;
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SM00179; EGF_CA;
SM00004; NL; 3.
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57; Conserv
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2; PS50297; ANK REP REGION; 1
3; PS00010; ASX HYDROXYL; 22.
4; PS00021; EGF 1; 34.
5; PS01186; EGF 2; 28.
6; PS01187; EGF CA; 21.
7r; Transcription regulation;
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in; Transmembrane; Glycoprotein;
                                                                                            PubMed=2574658;
born D., Hickok
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EGF-LIKE 6.
EGF-LIKE 9, CALCIUM-BINDING (EGF-LIKE 9. CALCIUM-BINDING (EGF-LIKE 10.
EGF-LIKE 11. CALCIUM-BINDING (EGF-LIKE 11.)
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                                                       J., Olsen D.R., Fazio M.J., utzmann R., Timpl R., Uitto J.; sequence and structural domains
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EMBL; X84819; CAA57709
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Timpl R., C
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MEDLINE=96044428; PubMed=7557988;
Zimmermann K., Hoischen S., Hafner M.,
"Genomic sequences and structural organ
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m; PF00008; EGF; 6.
m; PF00058; ldl recept b; 3.
m; PF00086; thyroglobulin_1; 1.
RT; SM00179; EGF_CA; 2.
RT; SM00682; G2F; 1.
RT; SM00135; LY; 5.
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L; X84821; CAA57709.

L; X84822; CAA57709.

L; X84823; CAA57709.

L; X84824; CAA57709.

L; X84825; CAA57709.

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L; X84827; CAA57709.

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L; X84829; CAA57709.

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L; X84831; CAA57709.

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SUBUNIT: Interacts with FBLN1 (By similarity).
SUBCELLULAR LOCATION: BASEMENT MEMBRANES.
PTM: N- AND O-GLYCOSYLATED.
SIMILARITY: Contains 6 EGF-like domains.
SIMILARITY: Contains 1 thyroglobulin type-I domain SIMILARITY: Contains 5 LDL-receptor YMTD domains.
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J. Hum. Genet. 44:876-885(1989).

FUNCTION: SULFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN BASEMENT MEMBRANES AND THAT IS TIGHTLY ASSOCIATED WITH LAMININ ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-
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1NDX; 29-DEC-
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IPR001881;
IPR006209;
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IPR000033;
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EGF_like.
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Thyroglobulin_1.
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R SMART; SM00211; TY; 1.

PROSITE; PS00010; ASX HYDROXYL; 3.

PROSITE; PS00484; HYDROGLOBULIN_1; 1.

DR PROSITE; PS00122; EGF_1; 1.

DR PROSITE; PS01116; EGF_2; 5.

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DR PROSITE; PS01116; EGF_1; 1.

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892
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                                                                                            833
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                                                                                                                                                                                                                                                                                                            67
                                                                                                                                                                                                                                                                                                                                                                                               20
                                                                                                                                                                                                                                                                                                                                                                                                                                            80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
      STGYCWCVDRDGR-EVEGTRTRPGMTPPCLSTVAPPIHQGPAVPTAVIPLP-PGTHLL--
                                                                                                                                      LSADGTLCVP
                                                                                                                                                                                                                     GSCVQPG----RCRCPAGWRGD--TCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHS
                                                                                                                                                                                                                                                                                                                                                TNAACRPGPRTQFTCECSIGFRGDGRTCYDIDECSE-----QP--SVCGSHTICNNH-
                                                                                                                                                                                                                                                                                                                                                                                           TEHAYRPGRRV-----CAVRAHG------DPVSESFVQRVYQPFLTTCDGHRACSTYR
                                                                                                                                                                            AQCIYTGGSSYTCSCLPGFSGDGQACQ-DVDECQPSRCHPDAFCYNTPGSFTCQCKPGY-
                                                                                                                                                                                                                                                                                                      TIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPP---CRNG-----
                                                                                       -QGDGFRCVPGEVEKTRCQHEREHILGAAGATDPQRPIPPGLFVPECDAHGHYAPTQCHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----VDSAMKEEVQRLQSRVDLLEEKLQLVLAPLH-SLASQALEHGLPDPGSLLVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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1115
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25.8%;
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                                                                                                                                                                                                                                                               PGTFRCECVEGYQFSD--EGTCVAVVDQRPINYCETGLHNCDIPQR
                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SULFATION (POTENTIAL).

BY SIMILARITY.

BY SIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    III (SMALLER GLOBÜLAR DOMAIN
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3, CALCIUM-BINDING
EGF-LIKE 4.
EGF-LIKE 5, CALCIUM-BINDING
THYROGLOBULIN TYPE 1.
LDL-RECEPTOR YWTD MOTIF 1.
LDL-RECEPTOR YWTD MOTIF 3.
LDL-RECEPTOR YWTD MOTIF 3.
LDL-RECEPTOR YWTD MOTIF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 173.5; DB 1
Pred. No. 6.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGF-LIKE 6
SULFATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          II (CYSTEINE-RICH).
III (SMALLER GLOBULAR DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I (LARGER GLOBULAR DOMAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                    ---KGGPPRVAPNPTG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                      98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .) (POTENTIAL).
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                                               243
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FBN1_MC
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Repeat;
SIGNAL
CHAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                              SWART; SW00179; EGF CA; 42.

PROSITE; PS00010; ASK HYDROXYL; 43.

PROSITE; PS00022; EGF 1; 2:

PROSITE; PS01186; EGF 2; 38.

PROSITE; PS01187; EGF CA; 43.

PROSITE; PS01187; EGF CA; 43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-CD-1; TISSUE-Kidney;

Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;

Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;

Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS

-I- FUNCTION: STRUCTURAL CONTAINING MICROFIBRILS PROVIDE

LONG-TERM FORCE BERRING STRUCTURAL SUPPORT.
                                                                                                                                                                                               InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR006209; EGF_like.
InterPro; IPR006212; Fibril-assoc.
Pfam; PF00008; EGF; 46.
Pfam; PF00683; TB; 9.
                                                                                                                                                                                                                                                                                                       EMBL; L29454; AAA56840.1;
EMBL; U22493; AAA64217.1;
PIR; A55624; A55624.
HSSP; P35555; 1APJ.
                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE MICROFIBRILS (BY SIMILARITY).
-!- SIMILARITY: Contains 47 EGF-like domains.
-!- SIMILARITY: Contains 7 TGF-beta binding protein (TGFB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FBN1 MOUSE STANDARD; PRT; 2871 AA. (51554; Q60826; Created) 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Primary structure and developmental fibrillin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95130561; PubMed=7829516;
Yin W., Germiller J., Sanguineti C.,
Pereira L., Ramirez F., Bonadio J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                            MGD; MGI:95489; Fbn1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FBN1 OR FBN-1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fibrillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244
                                                                                          Signal;
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; Multigene: 27
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                                                                                             family.
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POTENTIAL.
FIBRILLIN 1.
EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
EGF-LIKE 4,
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    CALCIUM-BINDING

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Smiley
                                                                                                                                                                                                                                                                                                                                                                                              noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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ch co							
Search completed: Job time : 25 secs	306	182	246	137	186	136	131
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Result .
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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222 HSLASQALEHGLP-DPGSLLVHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS	176 CVPKGGPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEK	116 SCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTL	57 DGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGA-AICQPPCRNGG -	1 MRGSOEVLLMWILLVIAVG-GTE-HAYRPGRRVCAVRAHGDPVSES	Query Match 28.9%; Score 435.5; Best Local Similarity 37.3%; Pred. No. 8.9e Matches 112; Conservative 36; Mismatches	A; Map position: 17 A; Introns: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3 A; Introns: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3 C; Superfamily: unassigned EGF-related proteins; EGF; 114-141/Domain: EGF homology < EGF1> F; 1148-183/Domain: EGF homology < EGF>	cession: T09065 atus: preliminary; translated from GB/EMBL/DDB: lecule type: DNA sidues: 1-293 <row> oss-references: EMBL:AF030001; NID:g2564945; PI</row>	ern, jor	cal protein - mou : Mus musculus () -Jun-1999	ALIGNMENTS	156 10.4 1408 2 155.5 10.3 466 1 155.5 10.3 3635 2 155 10.3 2471 2 154 10.2 387 2	158 10.5 1820 157 10.4 676 156 10.4 642 156 10.4 1221	10.7 2531 2 51818 10.6 2437 2 54261 10.5 407 1 KFBO7 10.5 456 1 KXBO	162 10.8 646 2 161 10.7 387 2 161 10.7 675 1	
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RESULT 2
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REST6 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

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RESULT 4
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R;Nakayama, M; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O. Genomics 51, 27-34, 1998
A;Title: Identification of high-molecular-weight proteins with multiple EGF-like A;Reference number: Z14126; MUID:98360089; PMID:9693030
A;Accession: T13954
A;Accession: T13954
      hypothetical protein Y64G10A.f - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #tex C;Accession: T27283 # R;Ainscapph, R.
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A;Experimental source: strain Sprague-Dawley; brain
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A; Residues: 1-1574 <NAK>
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                                                                                                                                                                                                                                                                                      YSRTCAMINCOYSCEDTEEGPOCLCPSSGLRLAPN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mewes, H.W.
ce Database,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 252.5; |
Pred. No. 3.8e
17; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 256; DB
Pred. No. 5.2e.
16; Mismatches
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                                                            15-Oct-1999 #text_change 15-Oct-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       September
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growth arrest-specific protein gas6 - human C;Species: Homo sapiens (man) C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Accession: B48089 C;Access
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C;Superfamily: notch protein; ankyrin C;Keywords: receptor; signal transduct F;514-545/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-1620 <WIL>
A; Residues: 1-1620 <WIL>
A; Cross-references: EWBL: AL110498; NID: e1542303; PIDN: CAB54471.1;
A; Cross-references: Clone Y64G10A
B48089
                   RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 22/1; 49/2; 148/1; 264/1; 1679/3; 1729/1; 1761/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: notch4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-1964
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A; Accession: T09059
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C;Date: 11-Jun-1999 #sequence_revisio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-1620 <1
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A;Reference number: Z20336
A;Accession: T27283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                 190 RDINECFLEPGPCPOGTSCHNTLGSYQCLCPVGQEGPQCKLRKGACPPGSCLNGGTCQLV
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                                                                                                                                                                                                                                                                                            80
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                                                                                                                                                                                                        SDVDECSARRGGCPQ--RCINTAGSYWCQC---WEGHSLSADGTLCVP----KGGPPRVA 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGSYWCQCWEGHSLSADGTLC-----VPKGG-PPRVAPNPTG 191
                                                                                   PEGHSTFHLCLCPPGFTGLDCEMNPD
                                                                                                                                                                                                                                                  ASGRPQCSCEPGWTGEQCQLRDFCSA----NPCANGGVCLATYPQIQCRCPPGFEGHTCE
                                                                                                                                                                                                                                                                                       APARPRYACCPGWK-RTSGLPGACGAAICQPPCRNGGSCVQPG---RCRCPAGWRGDTCQ 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                          signal transduction
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                                                                                                                                                                                                                                                                                                                                                       34.2%;
                                                                                                                                                                                                                                                                                                                                                                            13.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Library, October 1997
Library October 1997
the mouse major histocompatibility locus class III region.
                                                                                                                        TGVDSAMKEE 199
                                                                                                                                                                                                                                                                                                                                     12;
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                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.6e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                       Score 196; DB 2;
Pred. No. 1.6e-06;
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Pred. No. 3.2e-08;
9; Mismatches 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat homology;
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F;157-192/Domain:
                                                                                                                                                                                                                                                                               A;Gene: gas6
C;Superfamily: plasma protein S;
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F;242-297/Domain:
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A;Title: The protein encoded by a growth arrest-specific
                                                                                                                                                                                                                    F;198-233/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-678 < MAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                 ;Genetics:
                                                                                                                                                                                                                                                                    ;38-89/Domain:
                                                                                                                                                                                                       239-274/Domain:
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                                                                                                                                         Query Match
                                                                                                                                                                                     308-666/Domain:
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                                                                                                              50;
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein encoded by
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--PGW-KRTSGLPGAC------GAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDV
                                                RRAYQVFEEAKQGHLERECVEEVCSKEEA--REVFENDPETEYFYPRYQECMRKYGRPEE
                                                                             QRVYQPFLTTCDGH-----RACSTYRTIYRTAYRRSPGLAPARPRYACC------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SQENGGCLQICHNKPGSFHCSCHSGFELSSDGRTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SARRGGCPORCINTAGSYWCOCWEGHSLSADGTLC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNSGFATCVQNLPDQC----TPNPCDRKGTQACQDLMGNFFCLCKAGWGGRLCDKDVNEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRVYQPFLTTCDGH-----RACSTYRTIYRTAYRRSPGLAPARPRYACC----PGWK 93
                                                                                                                                                                                                                                 Gla domain homology #status
n: EGF homology <EG1>
n: EGF homology <EG2>
                                                                                                              Conservative
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                                                                                                                                                                     EGF homology <EG3>
EGF homology <EG4>
EGF homology <EG4>
sex hormone-binding globulin homology <SHB>
laminin G repeat homology <LGR>
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EGF homology <EG2>
EGF homology <EG3>
EGF homology <EG4>
EGF homology <EG4>
sex hormone-binding globulin homology <SHB>
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                                                                                                         Score 184; DB
Pred. No. 4.6e
8; Mismatches
                                                                                                                                                                                                                                                               EGF homology; Gla domain ogy #status atypical <GLA:
                                                                                                            8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 189; DB 2
Pred. No. 2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        growth arrest-specific
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                                                                                                                                                                                                                                                                                                                                                                                                                           PMID:8336730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G.; Schneider,
                                                                                                                           4.6e-06;
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r residue 424 as
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                                                                                                                                       Length 673;
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C;Accession: T10756
R;Kuroda, S
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S
                                                                                                 A;Residues: 1-810 <KUR>
A;Cross-references: EMBL:U48246; NID:g3851179; PID:g3851180
A;Experimental source: strain Sprague-Dawley, brain
                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                       A; Reference number: Z17122
A; Accession: T10756
                                                                                                                                                                                                                        R;Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Konishi, submitted to the EMBL Data Library, November 1998 A;Description: Protein kinase C-binding protein.
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A;Cross-references: GB:L39790; NID:g762830; C;Superfamily: fibrillin 1; EGF homology <EGF1>
F;1239-1274/Domain: EGF homology <EGF1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (house mouse)
C;Date: 23-Feb-1996 #sequence_revisio
C;Accession: A57278
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                                                                                                                                                       A; Molecule type: mRNA
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                                    Matches
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                                                                    Query Match
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Best Local
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 CCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGG
                                                                                                                                                                                                                                                                                                                                                                                                                      GHKQSETTQKC
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                                    Conservative
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                                                  12.0%;
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23.9%;
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                                                                                                                                                                                                                                                                                            revision
                                    13;
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                                                Score 180; DB 2;
Pred. No. 1.1e-05;
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Pred. No. 1.8e-05;
                                    Mismatches
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                                    38;
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                                                                    Length 810;
                                    Indels
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                                  Gaps
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growth potentiating f
C;Species: Rattus sp.
C;Date: 02-Jul-1996 #
C;Accession: 155476
                                                                                                          R;Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Hum. Mol. Genet. 2, 961-968, 1993
A;Title: Genomic organization of the sequence coding for fibrillin, A;Reference number: I54355; MUID:93372860; PMID:8364578
A;Accession: I54355
                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 02-Unn-1995 #sequence revision 25-Apr-1997 #text change 02-Aug-2002
C;Date: 02-Unn-1995 #sequence revision 25-Apr-1997 #text change 02-Aug-2002
C;Accession: A47221; 154355; S17064; I59574; S17062; S62111; A34198
R;Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
Genomics 17, 476-484, 1993
A;Title: Fibrilin binds calcium and is coded by cDNAs that reveal a multidomain structu
A;Reference number: A47221; MUID:94010947; PMID:7691719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:D42148; NID:g1526567; PIDN:BAA07719.1; PID:g8
C;Superfamily: plasma protein S; EGF homology; Gla domain homology;
F;29-89/Domain: Gla domain homology <GLA>
F;117-150/Domain: EGF homology <EG1>
F;157-192/Domain: EGF homology <EG2>
F;158-233/Domain: EGF homology <EG3>
F;39-274/Domain: EGF homology <EG3>
F;39-274/Domain: EGF homology <EG3>
F;39-274/Domain: EGF homology <EG4>
F;308-667/Domain: Sex hormone-binding globulin homology <SHB>
F;318-470/Domain: laminin G repeat homology <LGR>
                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-337, 'T', 339-1029 < COR>
A; Cross-references: GB: X63556
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A;Title: Vascular smooth muscle cell-derived, Gla-containing growth-potentiating A;Reference number: 155476; MUID:95197586; PMID:7890695
A;Accession: I55476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ś
A;Cross-references: GB:L13923; NID:g306745; R;Maslew, C.L.; Corson, G.M.; Maddox, B.K.;
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A; Residues: 1-674 < RES>
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                                                                                                                                                                                                                                                                                             A; Accession: A47221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fibrillin 1 precursor - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                            A; Residues: 132-3002 < PER >
                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10
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                                                                                       preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DECSARRGGCPORCINTAGSYWCOCWEGHSLSADGTLC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNPNFATCVKNLPDQCTPNPCDKKGTQLCQDLMGN-----PFCLCKDGWGGRLCDKDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHNYSRCVNLPGWYHCECRSGFHDDGTYSLSGESCI 595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.8%;
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Pred. No. 1.3e-05;
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PIDN:AAB02036.1; PID:g306746 Glanville, R.W.; Sakai, L.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 674;
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ology; laminin
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A;Map position: 15q21.1-15q21.1
A;Introns: 2236/1; 2258/1; 2207/*
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A,Title: Linkage of Martan syndrome and a phenotypically related disorder taleference number: S17062; MUID:91304567; PMID:1852206
A,Accession: S17062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; F;1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predictec F;132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC> F;1332-1367/Domain: EGF homology <EGF> F;1457-1492/Domain: EGF homology <EGF2> F;2362-2295/Domain: EGF homology <EGF1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 < LEE2
R; Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.
J. Biol. Chem. 264, 21381-21385, 1989
A; Title: Connective tissue microfibrils. Isolation and
A; Reference number: A34198; MUID: 90078246; PMID: 2512293
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R;Dietz, H.C.; Valle, D.; Franc
Science 259, 680-683, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 565-575;1890-1892,'I',1894-1900 .
C;Comment: Fibrillin is a major component of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: S62111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 'VLVTVVFIFLSYNKML',944-1444 <LEE1>
A;Cross-references: EMBL:X62008; NID:g31398; PIDN:CAB56534.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 2217-2288, 'I', 2290-2325 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1030-3002
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A;Title: Partial sequence of a candidate gene for the Marfan
A;Reference number: S17064; MUID:91304568; PMID:1852207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A34198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          PGGNQCIVPICRHSCGDGFCSR---PNMCTCPSGQIAPSCGS-RSIQHCNIRCMNGGSCS
NTVSSYFCKCPPGFYTSPDG
                                                                                                                                                            DVDECSARRGGCP-QRCINTAGSYWCQCWEGHSLSADGTLC--
                                                                                                                                                                                                                  CFTVISNQMCQGQLSGIVCTKQLCCATVGRAWGHPCEMCPAQPHPCRRGFIPNIRTGACQ
                                                                                                                                                                                                                                                                                                                              DDHCLCOKGYIGTH-----CGOPVCESGCLNGGRCVAPNRCACTYGFTGPQCERDYRTGP 316
                                                                                                                                                                                                                                                                                                                                                                                    RPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR----ACSTYRTIYRTAYRRSPGLAPA
                                                                                                         DVDECQAIPGLCQGGNCINTVGSFECKCPAGHKLNEVSQKCEDIDECSTIPGICEGGECT
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homology <EGF1>
                                                      PPRVAPNPTG 191
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22.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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C;Species: Gallus gallus (chicken)
C;Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change
C;Accession: A38963, Jp0076
R;Matsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.;
Dev. Dyn. 203, 212-222, 1995
A;Title: New gene, nel, encoding a Mr 93K protein with EGF-like
A;Reference number: A38963, MUID:95383734; PMID:7655083
A;Accession: A38963
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A; Residues: 1-835 < MAT>
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F;853-884/Domain: EGF homology <EGF3>
F;928-959/Domain: EGF homology <EGX4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;123-155/Domain: EGF homology <EGX1>
F;162-194/Domain: EGF homology <EGF1>
F;240-271/Domain: EGF homology <EGX2>
F;318-349/Domain: EGF homology <EGF>
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A;Residues: 1-2321 <JOU1>
A;Cross-references: EMBL:U97669; NID:g2668591; PIDN:AAB91371.1; PID:g2668592
R;Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabriat, H.; Mouton, P.;
x, M.M.; Weissenbach, J.; Bach, J.F.; Bousser, M.G.; Tournier-Lasserve, E.
Nature 383, 707-710, 1996
                                                                                                                                                                                                                                                                                              RESULT 13
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A;Residues: 67-113;138-194;268-333,'G',335-346;536-613;716-765;1240-1279;1815-1888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: EMBL:U97669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: S71825
                                                                                                                                                                                                                                             protein -
                                                                                                                                                                                                                                                                                                                                                                                                                      165
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                                                                                                                                                                                                                                                                                                                                                                                                                      EGHSLSADGTLCVPKGGPPRVAPNP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HGARCSVGPDGRFLCSCPPGYQGRSCRSDVDECRVGEPCRHGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGGSC-VQP-GR--CRCPAGWRGDTCQSDVDEC----SARRGGCPQRCINTAGSYWCQCW 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGRGVCQS-----SVVAGTARFSCRCPRGFRGPDCSLPDPC----LSSPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDGHRACSTYRTIYRTAYRRSPGLAPARPRYAC-CPGWKR--TSGLPGACGAAICOPPCR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     may be involved in pathogenesis of CADASIL, notch protein; ankyrin repeat homology; EGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                     -GPLCENPAVP--CAPSP
                                                                                                                                          S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.7%; Score 175.5; DB 2
34.5%; Pred. No. 5.7e-05;
tive 14; Mismatches 44
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                                                                                                                                                                                        24-Feb-1995 #text_change 13-Aug-1999
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                                                                                                                                            S.; Hori,
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A;Cross-references: EMB::M27445; NID:g602466; PIDN:AAA57261.1; PID:g602467 A;Note: the authors translated the codon AAG for residue 966 as Cys R;Fazio, M.J; O'Leary, J.; Kaehaeri, V.M.; Chen, Y.Q.; Saitta, B.; Uitto, J. Invest. Dermatol. 97, 281-285, 1991 A;Title: Human nidogen gene: structural and functional characterization of A;Reference number: A61367; MUID:91302882; PMID:1906509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Am. J. Hum. Genet. 44, 876-885, 1989
A;Title: Human nidogen: cDNA cloning, cellular expression, A;Reference number: A32437; MUID:89270475; PMID:2471408
A;Accession: A32437
                                                                A; Map position: 1q43-1q43
C; Superfamily: nidogen; EGF hor
C; Keywords: basement membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 20-Oct-2000 C;Accession: A33322; A32437; A61367
F;1-28/Domain: signal sequence #status predicted <SIG>F;29-1247/Product: nidogen #status predicted <MAT>
                                                                                                                                    A; Cross-references: GDB:120236; OMIM:131390
                                                                                                                                                            A;Gene:
                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-28 <FAZ>
C;Comment: This protein is a basement membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 667-1247 < OLS >
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A; Residues: 1-1247 < NAG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N; Alternate names: entactin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: 9-day embryo C; Superfamily: von Willebrand factor type C repeat homology; EGF homology F; 273-333/Domain: von Willebrand factor type C repeat homology < VWC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Matsuhashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; submitted to JIPID, January 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: DDBJ:D45365
A;Experimental source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A33322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Human nidogen:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Cross-references: EMBL:M30269;Olsen, D.R.; Nagayoshi, T.; Fem. J. Hum. Genet. 44, 876-885,
                                                                                                                                                                                 Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 GACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQR--CINTAG
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: EGF homology <EGF1>
: EGF homology <EGF>
: EGF homology <EGF2>
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A33322; MUID:90091745; PMID:2574658
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                                                              EGF homology; LDL receptor YWTD-containing repeat homology; thyr mbrane; beta-hydroxyasparagine; calcium binding; cell binding; co
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Pred. No. 3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M.; Mattei, M.G.; Passage,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.J.; Chu, M.L.;
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notch protein - fruit fly (Drosophila melanogaster)
N;Alternate names: neurogenic repetitive locus protein
C;Species: Drosophila melanogaster
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A24420; A24768; S09358; A05267
R;Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A;Reference number: A24420; MUID:87064624; PMID:3097517
A;Accession: A24420; MUID:87064624; PMID:3097517
A;Accession: A24420; MUID:87064624; PMID:3097517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
A24420
                                         Nucleic Acids Res. 17, 6463-6471, 1989
A;Title: Hypervariability of simple sequences as a general source for polymorphic DNA A;Paference number: S09358; MUID:89385974; PMID:2780284
                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-48,'I',50-118,'R',120-230,'I',232-256,'N',258-266,'A',268-872,'R',874-958.
A;Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 204'
                                                                                                                                                                                                                                                                             A;Residues: 1-2703 <KID>
A;Residues: 1-2703 <KID>
A;Cross-references: GB:K03508; NID:g157991; PIDN:AAA28725.1; PID:g157993
R;Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
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F;1076-1120/Domain: LDL receptor YWTD-containing repeat homology <YW3>
F;1121-1160/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;1121-1197/Domain: LDL receptor YWTD-containing repeat homology <YW4>
F;1121-1243/Domain: EDF receptor YWTD-containing repeat homology <YW5>
F;1212-1243/Domain: EGF homology <EG6>
F;229,296/Binding site: sulfate (Ty) (covalent) #status predicted
F;729,819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
F;756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin) #stat
F;1137/Binding site: carbohydrate (Asn) (covalent) #status predicted
                              A; Accession: S09358
                                                                                                                                                                                                                               A;Reference number: A24768; MUID:86079539; PMID:3935325 A;Accession: A24768
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                                                                                                                                R;Tautz, D
                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     762-800/Domain:
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714-750/Domain:
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lecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAQTGKIERL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STGYCWCVDRDGR-EVEGTRTRPGMTPPCLSTVAPPIHQGPAVPTAVIPLP-PGTHLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AQCIYTGGSSYTCSCLPGFSGDGQACQ-DVDECQPSRCHPDAFCYNTPGSFTCQCKPGY-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----VDSAMKEEVQRLQSRVDLLEEKLQLVLAPLH-SLASQALEHGLPDPGSLLVHS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -QGDGFRCVPGEVEKTRCQHEREHILGAAGATDPQRPIPPGLFVPECDAHGHYAPTQCHG
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cell attachment (R:
EGF homology <EG3>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 173.5;
Pred. No. 4.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: notch protein; ankyrin repeat homology; EGF homolog
C;Keywords: differentiation; tandem repeat; transmembrane protein
F;27-43/Domain: transmembrane #status predicted <TWM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 8.96-9.36
A; Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: opa: a novel family of transcribed repeats shared by the Notch locus and A;Reference number: A05267; MUID:85099329; PMID:2981631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 2505-2551,'QQQQ',2552-2576,'E',2578-2604 <TAU>
R;Wharton, K.A.; Yedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas,
Cell 40, 55-62, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;530-561/Domain: EGF homology <EGF1>F;568-599/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 2504-2576, 'E', 2578-2611 <WHA2>
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--TCVNTHGSYQCMCPTGYT---
                                           PORCINTAGSYWCQCWEGHSLSADGTLCVPKGGPPRVAPNP 189
                                                                                         GERCETKNICASSPCKNGATCTALAGSSSFTCSCPPGFTGDTCSYDIEECQSNPCKYGG-
                                                                                                                                                                                    HPGI----SCKCPLGFDESLCEIAVPNACDHVTCLNGGTCQLKTLEEYTCACANGYT
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                                                                                                                                                                                                                                                                           GGTCVTQLNGKTYCACDSHYVGD------YCEHRNPCNSMR-CQNGGTCQVTFRNG 118
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                      -QPPCRNGGSCV-----QPGRCRCPAGWRGDTCQSDVDECSA---RRGGC 148
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26.7%;
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Pred. No. 9.9e-05;
9; Mismatches 67
    GKDCDTKYKP--CSPSP
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Search completed: September 10, 2003, 17:15:38
Job time : 21 secs

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Result
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Perfect score:
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                        Sequence 37265, A Sequence 1532, Ap Sequence 1530, Ap Sequence 1830, App Sequence 1823, App Sequence 1823, Appl Sequence 41, Appl Sequence 41, Appl Sequence 2570, Ap Sequence 1941, Ap Sequence 4, Appl Sequence 2570, Ap Sequence 1861, Ap Sequence 1861, Ap Sequence 1861, Ap Sequence 176, Appl Sequence 176, Appl Sequence 176, Appl Sequence 1871, Appl Sequence 1871, Appl Sequence 1871, Appl Sequence 1817, A
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US-60-495-135-264	US-60-495-114-1137	US-60-487-610-2033	US-60-487-610-2032	US-60-487-610-2532	PCT-US02-38594-6	US-60-485-450-1176	US-09-908-576-4	US-60-495-135-409	US-60-495-135-408	US-60-495-114-1954	US-60-495-114-1953	PCT-US02-05093-6	US-60-485-450-1228	PCT-US03-24084-2	US-10-648-593-155	US-10-294-006-34	PCT-US02-24483-2	US-60-495-135-407
Sequence 264, App	Sequence 1137,	Sequence 2033,	Sequence 2032, .	Sequence 2532, 1	Sequence 6, Appli	Sequence 1176, 1	Sequence 4, Appl	Sequence 409, Ap	Sequence 408, App	Sequence 1954, F	Sequence 1953, Ap	Sequence 6, Appl	Sequence 1228, 1	Sequence 2, Appl	Sequence 155, App	Sequence 34, Appl	Sequence 2, Appli	Sequence 407, App

ALIGNMENTS

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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53313) B
CURRENT APPLICATION NUMBER: US/10/425,114A
CURRENT FILING DATE: 2003-04-28
INUMBER OF SEQ ID NOS: 73128
SEQ ID NO 37265
LENGTH: 285
LENGTH: 285
TYPE: PRT
ORGANISM: Homo sapiens
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Matches
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Davi
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Local Similarity 99.6%;
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VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS 273
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                                                                                                                                                                                                                   ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
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Pred. No. 1.7e-108;
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CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1530
LENGTH: 553
TYPE: PRT
ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-60-487-610-1532
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Best Local Similarity
Matches 57; Conserv
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CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1532
LENGTH: 436
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APPLICANT: HUANG, HONGJIN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIEROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
ETILE REFERENCE: CL001469
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APPLICANT: HUANG, HONGJIN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-II
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
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                   134 NSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLAPN 168
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                                                                                                                                        VOPGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCV 177
                                                                                                                                                                                  GNAASARHHGLLASA--ROPGVCHYGTKLACCYGWRRNS--KGVC-EATCEPGCK-FGEC
                                                                                                 VGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGHMLMPDAT-CV
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                                                                                                                                                                                                                                                                           Conservative
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                                                         -----RVAPN 188
                                                                                                                                                                                                                                                                    16.7%; Score 251.5; DB 7
36.8%; Pred. No. 3.8e-12;
ative 17; Mismatches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PKGGPP-----RVAPN 188
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Pred. No. 2.9e-12;
                                                                                                                                                                                                                                                                                                            DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7;
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                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                Length 553;
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                                                                                                                                                                                                                                                                    Gaps
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US-09-908-576-315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEO ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 315, Application US/09908576 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1531, Application US/60487610 GENERAL INFORMATION:
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               APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/908,576
CURRENT FILING DATE: 2001-07-18
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APPLICANT: HUANG, HONGJIN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-I
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Genentech, Inc. APPLICANT: Ashkenazi, Avi
PRIOR APPLICATION NUMBER: US/09/665,350B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 Match 16.7%; Score 251.5; DB 7 Local Similarity 36.8%; Pred. No. 3.9e-12; Press 57; Conservative 17; Mismatches 50
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                                                                                                                                                                                                                                                                 Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGHMLMPDAT-CV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNAASARHHGLLASA--ROPGVCHYGTKLACCYGWRRNS--KGVC-EATCEPGCK-FGEC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                       Fong, burners Gao, Wei-Qiang
                                                                                                                                                             Stewart, Timo
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                               Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                             Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                      Roy, Margaret Ann
                                                                                                                                                                                                                          Paoni,
                                                                                                                                                                                                                          Nicholas F.
                                                                                                                                                                               Timothy A.
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FILING DATE: 2000-09-18
APPLICATION NUMBER: PCT/US00/04414

FILING DATE:

2000-02-22

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                                                                                                                                                                                                                                                                              ; LENGTH: 2003
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1823
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                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 1823
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Best Local Similarity 42.4
Matches 42; Conservative
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LENGTH: 509
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                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: CARGILL, Michele
APPLICANT: HUANG, HONGJIN
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-I
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
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CURRENT FILING DATE: 2003-07-17
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                Match 12.5%; Score 188.5; DB 7; Local Similarity 29.6%; Pred. No. 1.1e-06;
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APPLICATION NUMBER: PCT/US99/20944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1999-07-07
                                                                                                                       137
192 VDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPD----PGSLLVHSFQQL 247
                                       193 RDVNECFODPGPCPKGTSCHNTLGSFQCLCPVGQ----EGPRCELRAGPCPPRGCSN-GG
                                                                            136 SDVDECSARRGGCPQ--RCINTAGSYWCQCWEGHSLSADGTLCVPKGG--PPRVAPNPTG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 SDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGT 174
                                                                                                                                                        80 APARPRYACCPGWK-RTSGLPGACGAAICQPPCRNGGSCVQPG---RCRCPAGWRGDTCQ 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                                                                                   ASGRPQCSCMPGWTGEQCQLRDFCSA----NPCVNGGVCLATYPQIQCHCPPGFEGHACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQ 135
                                                                                                                                                                                                    Conservative
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42.4%; Pred. No. 5.4e-10;
ative 13; Mismatches 40
                                                                                                                                                                                                  17; Mismatches
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CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US 60/323,469
PRIOR FILING DATE: 2001-09-17
NUMBER OF SEQ ID NOS: 412
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 361
LENGTH: 810
                                                                                                                                                                                                                                                                                                                                                      Sequence 41, Application PC/TUS0325418 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                     APPLICANT: INCYTE CORPORATION APPLICANT: ELLIOTT, Vicki S.
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APPLICANT:
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TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-002710PC
                                                                                                                                                                                                                                                                       APPLICANT:
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      148 C--PORCINTAGSYWCOCWEGH----SLSADGTLCV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       504 CKPGYVGN----GTICRAFCEEGCRYGGTCVAPNKCVCPSGFTGSHCEKDIDECSEGIIE 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 GTCQDGLDTYTCLCPETWTGWDCSED 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88 CCPGWKRTSGLPGACGAAICOPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36;
BLAKE, Julie J.
WANG, Jonathan T.
CHIEN, David
YANG, Yonghong G.
                                                                                                                                                                                                                           TRAN, L.
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Mack, David H.
Wilson, Keith E.
Zlotnik, Albert
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Gish, Kurt C.
                                                                   JACKSON, Alan A. RICHARDSON, Thom
                                                                                                                                                                                  MARQUIS, Joseph P. SWARNAKAR, Anita
                                                                                                                                                                                                                                                  EMERLING, Brooke M. KABLE, Amy E. TRAN, Uyen K.
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KHARE, Reena
                                                                                                                                   RAMKUMAR, Jayalaxmi
HAFALIA, April J.A.
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                                                                                                                                                                      CHAWLA, Narinder K.
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Pred. No. 1.3e-06;
.2; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 810;
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RESULT 9
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Best Local S
Matches 67
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SEQ ID NO 41
LENGTH: 366
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                                                                       APPLICANT
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PRIOR APPLICATION NUMBER: US 60/413,890
PRIOR FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 60/424,904
PRIOR APPLICATION NUMBER: US 60/424,904
PRIOR FILING DATE: 2002-11-08
                                                                                                                                                                             APPLICANT:
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NUMBER OF SEQ ID NOS: 84
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PRIOR APPLICATION NUMBER: US 60/410,566
PRIOR FILING DATE: 2002-09-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/407,034
                                                      APPLICANT
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OTHER INFORMATION: Incyte ID No: 7522915CD1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 60/426,222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62 CSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSG--LP---GACGAAICOPPCRNGGS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 LLLLALGHTWTYREEPQDGDREIC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 LLVLAVGGT----EHAYRPGRRVCAVRAHGDPVSESFVQRVYQPF-----LTTCDGHRA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
67; Conserv
        SWARNAKAR, Anita
CHAWLA, Narinder K.
RAMKUMAR, Jayalaxmi
HAFALIA, April J.A.
LEE, Soo Yeun
JIANG, Xin
                                                                                                                                                                                                                                                                                                                                                                                                                                              ALL 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHSLSADGTLCVPKGGPPRVAPNPTGVDSA--
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                                                                                                                                                                TRAN, U,
                                                                                                                               MARQUIS, Joseph P.
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EMERLING, Brooke M.
                                                                                                                                                                                          KABLE, Amy E.
TRAN, Uyen K.
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                                                                                                                                                                                                                                                                              Vicki S.
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US-60-490-890-481
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PRIOR FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US 60/407,034
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/410,566
PRIOR FILING DATE: 2002-09-13
PRIOR FILING DATE: 2002-09-24
PRIOR FILING DATE: 2002-09-24
SOFTWARE: PatentIn version 3.2
SEQ ID NO 481
LENGTH: 2871
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Best Local (
                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                            TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION FILE REFERENCE: D0310 PSP CURRENT APPLICATION NUMBER: US/60/490,890 CURRENT FILING DATE: 2003-07-29 NUMBER OF SEQ ID NOS: 2779
                                                                                                                                                                                                                              APPLICANT: Li, Martha APPLICANT: Rupnow, Bi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/426,222
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 84
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CURRENT FILING DATE: 2003-08-12
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APPLICANT: YANG, Yonghong G.
TITLE OF INVENTION: CELL ADHE
FILE REFERENCE: PF-1500 PCT
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TYPE: PRT
ORGANISM: Homo sapiens
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OTHER INFORMATION: Incyte ID No: 7513607CD1
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                                                                                                                                                                                                                                                                                                                                                                                                 261 NVSYVKTSPFOCERNPCPMDS 281
                                                                                                                                                                                                                                                                                                                                                                                                                                        174 TLCVPKGGPPRVAPNPTGVDS 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 SCEAGFHLSGAAGDSVCQDVDECVGLQPVCPQGTTCINTGGSFQCVSPECPEG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 RCPAGWR-----GDTCQSDVDECSARRGGCPQ--RCINTAGSYWC----QCWEGHSLSADG 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55
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                                                                                                                                                                  Rupnow, Brent A. Webster, Kevin R. Jackson, Donald Wong, Tai W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPADGRKFGSKYLVDHEVHFTCNPGFRLVGPSSVVCLPNGTWTGEQPHCRGISECSSQPC 145
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27.4%;
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16;

Score 176.5; DB 1 Pred. No. 1.5e-06; Mismatches

DB 1;

393;

Indels Length

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Gaps

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; ORGANISM: Hom
US-60-490-890-481
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US-60-487-610-1941
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US-60-487-610-1941
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                                                                                                                                       Sequence 2570, Application US/60487610 GENERAL INFORMATION:
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APPLICANT: HUANG, Hongiin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1941
LECT.
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Best Local Similarity
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APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Hongjin
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: HETHORS IN HEPATITIS C VIRUS-1
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
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                                                                                                                                                                                                                                                                                                                                        625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1587
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                                                                                                                                                                                                                                                                                                                                                                                                                   39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR----ACSTYRTIYRTAYRRSPGLAPA
                                                                                                                                                                                                                                                             ECAQEPPPCGPGRCDNTAGSFHCACPAGFRSRGPGAPC 713
                                                                                                                                                                                                                                                                                               ECSARRGGC-PORCINTAGSYWCOCWEGHSLSADGTLC 176
                                                                                                                                                                                                                                                                                                                                        AAPHGASCQDVDECTQSPGLCGRGACKN--
                                                                                                                                                                                                                                                                                                                                                                            ARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPG--RCRCPAGWRGDTCQSDVD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVDECQAIPGLCQGGNCINTVGSFECKCPAGHKLNEVSQKCEDIDECSTIPGICEGGECT 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVDECSARRGGCP-QRCINTAGSYWCQCWEGHSLSADGTLC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CFTVISNQMCQGQLSGIVCTKTLCCATVGRAWGHPCEMCPAQPHPCRRGFIPNIRTGACQ 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGNQCTVPICRHSCGDGFCSR---PNMCTCPSGQIAPSCGS-RSIQHCNIRCMNGGSCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 11.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PPRVAPNPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                 6,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 176; DB 7; Length 1587; Pred. No. 7.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191
                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                          AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                        --LPGSFRCVCPAGFRGSACEEDVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79;
                                                                                                                                                                                                                                                                                                                                                                                                                 41; Indels
                                                              VIRUS-INFECTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----VPKGG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----S
                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBJECTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130
                                                                                                                                                                                                                                                                                                                                        675
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CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOPTMARE: PASTSEQ for Windows Vers
SEQ ID NO 2570
LENGTH: 2321
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-2570
                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: VIRUS INFECTED SUBJECTS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOI470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1335
LENGTH: 671
TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 13
US-60-485-450-1335
(Sequence 1335, Application US/60485450
; GENERAL INFORMATION:
   APPLICANT: CARCILL, Michele
   APPLICANT: CHANG, Sheng-Yung
   TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
   TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN I
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                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                            Match 11.6%; Score 175; DB 7; J
Local Similarity 33.1%; Pred. No. 3.5e-06;
les 60; Conservative 10; Mismatches 57;
                                                                                                                                                         338
                                      182
                                                                                                                                                                                                                                     307
456
                                                                           396 GPGEGACQDVDECALGRSPCAQGCTNTDGSFHCSCEEGYVLAGEDGTQCQDVDECVGPGG
                                                                                                              131 --GDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSA-DGTL-----CVPKGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 HGARCSVGPDGRFLCSCPPGYQGRSCRSDVDECRVGEPCRHGG---TCLNTPGSFRCQCP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 NGGSC-VQP-GR--CRCPAGWRGDTCQSDVDEC----SARRGGCPQRCINTAGSYWCQCW 164
                                                                                                                                                                                            79 LAPARPRYAC-CP-GWKRTSGLPGACGAAICQ-PPCRNGGSCVQ-PG--RCRCPAGWR-- 130
                                                                                                                                                                                                                                                                          25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56 CDGHRACSTYRTIYRTAYRRSPGLAPARPRYAC-CPGWKR--TSGLPGACGAAICQPPCR 112
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                                      שי
                                                                                                                                                                                                                                                                        RPGRRV-----CAVRAHGDPVSESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPG
                                                                                                                                                         LGPHGKNYTCRCPQGYQLDSSQLDCVDVDECQDSPCAQ--ECVNTPGGFRCECWVGYEPG 395
                                                                                                                                                                                                                                     RPGFRLLDDLVTCASR --- NPCSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGHSLSADGTLCVPKGGPPRVAPNP 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGRGVCQS------SVVAGTARFSCRCPRGFRGPDCSLPDPC----LSSPCA 129
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                                      182
456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GPLCENPAVP--CAPSP 205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESPONSE TO INTERFERON TREATMENT IN HEPATITIS VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 175.5; DB 7
; Pred. No. 1.3e-05;
14; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44; Indels 37;
                                                                                                                                                                                                                                                                                                                                                   Length 671;
                                                                                                                                                                                                                                                                                                                 Indels
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RESULT 14
US-60-487-610-2260
(Sequence 2260, Application US/60487610)
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele

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                                                                                      PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR PPLICATION NUMBER: 60/323,994
PRIOR APPLICATION NUMBER: 60/323,994
PRIOR APPLICATION NUMBER: 60/373,814
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR APPLICATION NUMBER: 60/310,291
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-03
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-09
PRIOR PILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/310,544
PRIOR FILING DATE: 2001-08-07
PRIOR PILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/311,292
PRIOR FILING DATE: 2001-08-09
PRIOR FILING DATE: 2001-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application PC/TUS0224483
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2260
DENOTH: 1247
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: PCT/US02/24483
CURRENT FILING DATE: 2002-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CuraGen Corp. et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES,
FILE REFERENCE: 21402-416A-061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIEROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
APPLICATION NUMBER: 60/312,892 FILING DATE: 2001-08-16
                                                FILING DATE:
                                                                 APPLICATION NUMBER: 60/313,201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 LSADGTLCVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        681 TNAACREGERTQFTCECSIGFRGDGRTCYDIDECSE-----QP--SVCGSHTICNNH-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 TEHAYRPGRRV-----CAVRAHG------DPVSESFVQRVYQPFLTTCDGHRACSTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QGDGFRCVPGEVEKTRCQHEREHILGAAGATDPQRPIPPGLFVPECDAHGHYAPTQCHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAQTGKIERL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STGYCWCVDRDGR-EVEGTRTRPGMTPPCLSTVAPPIHQGPAVPTAVIPLP-PGTHLL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AQCIYTGGSSYTCSCLPGFSGDGQACQ-DVDECQPSRCHPDAFCYNTPGSFTCQCKPGY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSCVQPG----RCRCPAGWRGD--TCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHS 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPP---CRNG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----VDSAMKEEVQRLQSRVDLLEEKLQLVLAPLH-SLASQALEHGLPDPGSLLVHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                2001-08-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------KGGPPRVAPNPTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Mismatches
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Pred. No. 9.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACIDS ENCODING SAME, AND METHOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1247;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               891
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SOFTWARE CUraSeqList version 0.1
SEQ ID NO 4
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                                                                                                                   ECVT---SSCEGHCVNTEGGFVCECGPGMQLSADRHSCQDTDECLGTPCQQRCKNSIGSYK
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266
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24.1%; Pre
24.1%; 16;
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Search completed: September 10, 2003, 17:23:33 Job time : 22 secs

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Result
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Copyright (c) 1993 - 2003
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ALIGNMENTS

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RESULT 1
PCT-US99-08900-2
; Sequence 2, Application PC/TUS9908900
; GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE T125-RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/074W01
; CURRENT APPLICATION NUMBER: PCT/US99/08900
; CURRENT FILING DATE: 1999-04-23
; EARLIER APPLICATION NUMBER: US 09/065,363
; EARLIER FILING DATE: 1998-04-24
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 273
; TYPE: PRT
GORGANISM: Homo sapiens
PCT-US99-08900-2

Query Match
Best Local Similarity 100.0%; Score 1505; DB 1; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.6e-113;
Matches 273; Conservative 0; Mismatches 0; Gaps
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Matches 273
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                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 273 amino acids
                                                                                                                                                                           MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOLTZMAN, TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                      NAME: Meiklejohn, Ph.D., An REGISTRATION NUMBER: 35,283 REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23-APR-1998 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
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STRY: Boston
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TOPOLOGY:
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ZIP: 02110-2804
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ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP 120
                                                            MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR 60
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                                                                                            100.0%; Score 1505; DB 14; 100.0%; Pred. No. 4.6e-113; tive 0; Mismatches 0;
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GENERAL INFORMATION:
APPLICANT: Holtzman,
TITLE OF INVENTION: F
TITLE OF INVENTION: F
NUMBER OF SEQUENCES:
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                   Matches 273;
                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                             MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-APR-1998 PRIOR APPLICATION DATA:
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MEDIUM TYPE: Diskette
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ADDRESSEE: Fish & Richardson P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meiklejohn, Ph.D., REGISTRATION NUMBER: 35,
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SOFTWARE: FastSEQ
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STREET: 225 Franklin Street
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SYSTEM: Windows95
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PROTEIN FAMILY AND USES THEREOF
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Pred. No. 4.6e-113;
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US-09-298-531-2
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GENERAL INFORMATION:
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LENGTH: 273
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                     FILE REFERENCE: P2630R1E
CURRENT APPLICATION NUMBER: US/09/380,138
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: PCT/US99/05028
PRIOR FILING DATE: 1999-03-08
                                                              APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding
FILE REFERENCE: P2630R1E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/298,531
CURRENT FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: US 09/065,363
EARLIER FILING DATE: 1998-04-25
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TITLE OF INVENTION: NOVEL MOLECULES OF
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/074001
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SOFTWARE: FastSEQ for Windows Version 3.0
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 FILING DATE:
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Gurney, Austin
Yuan, Jean
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Pred. No. 4.6e-113;
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          APPLICATION NUMBER: US
FILING DATE: 1998-04-1
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APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Yuan, Jean
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Novel Polypeptides and
FILE REFERENCE: P2630R1E
CURRENT APPLICATION NUMBER: US/09/380,138
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Pred. No. 4.6e-113;
; Mismatches 0;
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APPLICATION NUMBER:

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N: US 60/077,632 1998-03-11

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US 60/081,955

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APPLICATION NUMBER: 1998-04-01 APPLICATION NUMBER: 1998-04-01 APPLICATION NUMBER: US FILING DATE: 1998-04-01 APPLICATION NUMBER: 1998-04-01 FILING DATE: 1998-03-31
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60/080,333

APPLICATION NUMBER: 1998-03-30

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APPLICATION NUMBER:
1998-03-27

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APPLICATION NUMBER: US 60/078,004 FILING DATE: 1998-03-13

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NUMBER OF SEQ ID NO;
SEQ ID NO 508
LENGTH: 273
Sequence 10, Application US/09790264
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: McCarthy, Sean A.
'TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE,
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RESULT 8
US-09-108-585A-506
; Sequence 506, Application US/09918585A
; GENERAL INFORMATION:
; APPLICANT: Bakker Kevin P.
; APPLICANT: Botstein, David

APPLICANT:

APPLICANT:

APPLICANT: APPLICANT: APPLICANT:

Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L.

APPLICANT:

Gao, Wei-Qiang Filvaroff, Ellen Eaton, Dan Desnoyers, Luc

APPLICANT: APPLICANT:

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PRIOR APPLICATION NUMBER: US 09/065,661
PRIOR FILING DATE: 1998-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 09/065,363
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILING DATE: 1998-06-22
PRIOR PRILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR PILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR PILING DATE: 1998-07-29
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CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21
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NAME/KEY: SIGNAL
LOCATION: (1)...(22)
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          R FILING DATE: 1998-03-31
R APPLICATION NUMBER: 60/080165
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R APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/079786
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APPLICATION NUMBER: 60/065311
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Wood, William I.
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RESULT 9
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APPLICANT: Baker Kevin P.
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APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/085689
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                                              Botstein, David
Desnoyers, Luc
  Ferrara,
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APPLICAN: NULLER, Mickey
APPLICAN: WOOd, William, P. Mickey
APPLICAN: WOOd, William, P. Mickey
APPLICAN: WOOd, William, P. Mickey
APPLICAN: Wood, William, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
TILL REPRENCE: P5630PC1
CURRENT PILLING DATE: 2500PC1
PRIOR PILLING DATE: 1997-10-17
PRIOR PILLING DATE: 1997-10-17
PRIOR PILLING DATE: 1997-10-17
PRIOR PILLING DATE: 1997-11-3
PRIOR APPLICATION NUMBER: 60/06534
PRIOR FILLING DATE: 1997-11-3
PRIOR APPLICATION NUMBER: 60/077450
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Williams, P. Mi
Wood, William J
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Shelton, David L.
Stewart, Timothy A.
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Gerber,
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Goddard, Audrey
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Sophia S.
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PRIOR APPLICATION NUMBER: 60/084411
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NUMBER: 60/080328 NUMBER: 60/080327 NUMBER: 60/080194 1998-03-31

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US-09-978-187B-506; Sequence 506, App.; GENERAL INFORMAT
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CURRENT FILING DATE: 2001-10-15
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PRIOR FILING DATE: 2001-07-30
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                                                   APPLICATION NUMBER: 60/079656 FILING DATE: 1998-03-26
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Botstein, David
Desnoyers, Luc
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Wood, William
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
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ms, P. Mickey
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APPLICATION NUMBER: 60/081049
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FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079728
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083496 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 AFFLIANG DATE: 1998-04-08
AFFLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
AFFLICATION NUMBER: 60/081203 APPLICATION NUMBER: 60/080333 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334 APPLICATION NUMBER: 60/080327 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080328 FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080107
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080165 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082700 APPLICATION NUMBER: 60/081229 FILING DATE: 1998-03 APPLICATION NUMBER: FILING.DATE: 1998-03 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/082797 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081819 FILING DATE: 1998-04-15 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081071 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-30 APPLICATION NUMBER: 60/079923 LING.DATE: 1998-03-31 1998-04-29 1998-04-28 1998-04-22 1998-04-21 1998-04-15 1998-03-30 1998-04-15 1998-04-15 1998-03-31 1998-03-27 60/082568 60/083499 60/083392 60/082704 60/081838 60/081952 60/081817 60/081955 60/080194 60/079920

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APPLICATION NUMBER: 60/085573
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/084627
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APPLICATION NUMBER: 60/084643
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                               GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1CS
CURRENT EPLICATION NUMBER: US/09/978,187B
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1907-10-17
PRIOR APPLICATION NUMBER: 60/06220
PRIOR APPLICATION NUMBER: 60/06231
PRIOR APPLICATION NUMBER: 60/064249
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APPLICATION NUMBER: 60/078004
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Baker Kevin P.
Botstein, David
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Kuo, Sophia S.
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60/081229

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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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Gerritsen, Mary E.
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Hillan, Kenneth J
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Grimaldi, J. Christopher
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C8
CURRENT APPLICATION NUMBER: US/09/978,188A
CURRENT FILING DATE: 2001-10-15
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Botstein, David
Desnoyers, Luc
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Williams, P. Mickey
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Shelton, David L.
Stewart, Timothy A.
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Gerritsen, Mary
Goddard, Audrey
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Napier, Mary A.
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Grimaldi, J. Christopher
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Filvaroff,
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sen, Mary E.
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APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728

APPLICATION NUMBER: FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-27

60/079689 60/079664

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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Pani, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC7
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US/09/978,189
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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APPLICANT: Ashkenazi, Avi
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Best Local Similarity
Matches 273; Conserv
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Cao, Wei-Qiang
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Hillan, Kenneth J
Kljavin, Ivar J.
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                                          Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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PRIOR APPLICATION PRIOR FILING DATE: PRIOR FILING DATE: 1998-0 PRIOR APPLICATION NUMBER: PRIOR PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR-FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085689
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085704
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/0
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                     VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
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VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
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Pred. No. 4.6e-113;
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RESULT 15
US-09-978-189-508
Sequence 508, Applicat
Sequence INFORMATION: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT APPLICANT: APPLICANT: APPLICANT APPLICANT: APPLICANT: APPLICANT: : Ashkenazi, Avi : Baker Kevin P. : Botstein, David : Desnoyers, Luc Fong, buccang Gao, Wei-Qiang Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A Kljavin, Ivar J. Kuo, Sophia S. Napier, Mary A. Gerber, Hanspeter Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J. Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J Kljavin, Ivar J. Kno. Somhia S. Ferrara, Napoleon Filvaroff, Ellen Eaton, Application US/09978189 James; Dan Ħ

PRIOR FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080194 PRIOR FILING DATE: 1998-03-31 PRIOR APPLICATION NUMBER: 60/080327 PRIOR APPLICATION NUMBER: 60/080327 PRIOR APPLICATION NUMBER: 60/080328 PRIOR FILING DATE: 1998-04-01 PRIOR PRILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/080333 PRIOR FILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/080334 PRIOR APPLICATION NUMBER: 60/080334 PRIOR APPLICATION NUMBER: 60/080336 PRIOR PILING DATE: 1998-04-01 PRIOR APPLICATION NUMBER: 60/080336 PRIOR FILING DATE: 1998-04-01 PRIOR FILING DATE: 1998-04-08	APPLICATION N FILLING DATE: APPLICATION N FILLING DATE:	Mic ted 1-1
PRIOR APPLICATION NUMBER: 60/084411 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084411 PRIOR FILING DATE: 1998-05-06 PRIOR APPLICATION NUMBER: 60/084637 PRIOR FILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084639 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR PILING DATE: 1998-05-07 PRIOR APPLICATION NUMBER: 60/084640 PRIOR APPLICATION NUMBER: 60/084600	PRIOR APPLICATION NUMBER: 60/081229 PRIOR FILING DATE: 1998-04-09 PRIOR APPLICATION NUMBER: 60/081955 PRIOR APPLICATION NUMBER: 60/081817 PRIOR APPLICATION NUMBER: 60/081817 PRIOR APPLICATION NUMBER: 60/081817 PRIOR FILING DATE: 1998-04-15 PRIOR APPLICATION NUMBER: 60/081819 PRIOR APPLICATION NUMBER: 60/081819 PRIOR APPLICATION NUMBER: 60/081838 PRIOR FILING DATE: 1998-04-21 PRIOR APPLICATION NUMBER: 60/082569 PRIOR APPLICATION NUMBER: 60/082569 PRIOR APPLICATION NUMBER: 60/082704 PRIOR APPLICATION NUMBER: 60/082704 PRIOR APPLICATION NUMBER: 60/082704 PRIOR APPLICATION NUMBER: 60/082704 PRIOR APPLICATION NUMBER: 60/082704 PRIOR APPLICATION NUMBER: 60/082704 PRIOR APPLICATION NUMBER: 60/082706 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/082797 PRIOR APPLICATION NUMBER: 60/083336 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083392 PRIOR APPLICATION NUMBER: 60/083499 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594 PRIOR APPLICATION NUMBER: 60/083594	APPLICATION NUMBER: FILING DATE: 1998-0. APPLICATION NUMBER: FILING DATE: 1998-0. APPLICATION NUMBER: FILING DATE: 1998-0. APPLICATION NUMBER: FILING DATE: 1998-0.

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OR APPLICATION NUMBER: 60/085582
OR FILING DATE: 1998-05-15
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Search completed: September 10, 2003, 17:23:05
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US-09-998-32A-508
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US-09-978-189-508
US-09-978-189-508
US-09-978-608A-508
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US-09-978-585A-506
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Sequence 10, Appl Sequence 506, App Sequence 508, App
                                                                                                                                                                                                                                                                                                                      Description
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ALIGNMENTS

US-09-790-264-10 RESULT 1

Sequence 10, Application U Patent No. US20020028508A1 GENERAL INFORMATION:

Application US/09790264

US-09-790-264-10 PRIOR APPLICATION NUMBER: US 09/065,661
PRIOR FILLING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/298,531
PRIOR FILLING DATE: 1999-04-23
PRIOR FILLING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 09/065,363
PRIOR FILLING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: US 09/337,930
PRIOR FILLING DATE: 1999-06-22
PRIOR APPLICATION NUMBER: US 09/102,705
PRIOR FILLING DATE: 1998-06-22
PRIOR FILLING DATE: 1998-06-22
PRIOR FILLING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR APPLICATION NUMBER: US 09/363,630
PRIOR FILLING DATE: 1998-07-29
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR APPLICATION NUMBER: US 09/124,538
PRIOR APPLICATION NUMBER: US 09/124,538 NUMBER OF SEQ ID NOS: 68 SOFTWARE: FastSEQ for Windows SEQ ID NO 10 APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Goodearl, Andrew D.J.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES
FILE REFERENCE: 07334-322001
CURRENT APPLICATION NUMBER: US/09/790,264
CURRENT FILING DATE: 2001-02-21 NAME/KEY: SIGNAL LOCATION: (1)...(22) TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: LENGTH: 273

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RESULT 2
US-09-97
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Pol
TITLE OF INVENTION: Acids Encoding the Same
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PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
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   FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066364
FILING DATE: 1997-11-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
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                                                                                                                                                                                                                                                                                                                                                               Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                             Hillan, Kenneth J
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Grimaldi, J. Christopher
Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerritsen, Mary E
Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eaton,
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Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09978295A
                                                                                                                                                                                                                                                                                                                                                                                              javin,
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i, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wei-Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sherman
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                                                                                                                                                                                                                                                                                                                                                                                              Ivar J.
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Prèd. No. 1.5e-114;
); Mismatches 0;
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PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
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OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079728
              APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081819
FILING DATE: 1998-04-15
                                                                                           APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
                                                                            FILING DATE:
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FILING DATE: 1998-04-08
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FILING DATE: 1998-0
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
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APPLICATION NUMBER: 60/078939
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
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FILING DATE: 1998-03-11
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DR APPLICATION NUMBER: 60/084366
OR FILING DATE: 1998-05-05
OR FILING DATE: 1998-05-06
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OR APPLICATION NUMBER: 60/084640
DR APPLICATION NUMBER: 60/085582

DR FILING DATE: 1998-05-15

DR APPLICATION NUMBER: 60/085700

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DR APPLICATION NUMBER: 60/085689

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APPLICATION NUMBER: 60/
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FILING DATE: 1998-05-07
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083742
FILING DATE: 1998-04-30
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
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APPLICATION NUMBER: 60/083545
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APPLICATION NUMBER: 60/083554
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
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APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/082797
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PRIOR APPLICATION NUMBER: 60/085573
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PRIOR APPLICATION NUMBER: 60/085704
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                                                            APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C11
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APPLICANT:
                    CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
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APPLICANT: Baker Kevin P.
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Gerritsen, Mary E.
Gedard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Kuo, Sophia S.
Napier, Mary A.
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Botstein, David
Desnoyers, Luc
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Filvaroff, Ellen
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OR FILING DATE: 1998-03-11

FILING DATE: 1997-11-03 APPLICATION NUMBER: 60/065311 FILING DATE: 1997-11-13

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APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/064249

OR APPLICATION NUMBER: 60/077641

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OR APPLICATION NUMBER: 60/077649

OR FILING DATE: 1998-03-11

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OR APPLICATION NUMBER: 60/079664
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DR FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080327

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APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081070

OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079923
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Grimaldi, J. Christopher
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                Margaret Ann
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Kenneth J
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PRIOR APPLICATION NUMBER: 60/077632
PRIOR APPLICATION NUMBER: 60/077641
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR PRIOR PAPELICATION NUMBER: 60/077649
PRIOR PRIOR APPLICATION NUMBER: 60/07791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078066
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PRIOR APPLICATION NUMBER: 60/079294 FILE REFERENCE: P2630P1C27

CURRENT APPLICATION NUMBER: US/09/978,697

CURRENT FILING DATE: 2001-10-16

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/064249

PRIOR APPLICATION NUMBER: 60/064249 PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/65311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077450
PRIOR PILING DATE: 1998-03-10 PRIOR APPLICANT: APPLICANT: Wood, WITITLE OF INVENTION: OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079920
OR FILING DATE: 1998-03-30
OR APPLICATION NUMBER: 60/079923
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OR APPLICATION NUMBER: 60/080107 FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/079728 FILING DATE: 1998-03-26 APPLICATION NUMBER: 60/079664 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079689 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60 FILING DATE: 1998-03-3 APPLICATION NUMBER: 60/080334 FILING DATE: 1998-04-01 FILING DATE: 1998-03-31 INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Williams, P. N Wood, William Tumas, Daniel NUMBER: P. Mickey 60/080327 60/080194 60/080165 Encoding the Same

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OR APPLICATION NUMBER: 60/082796
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OR APPLICATION NUMBER: 60/083336
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OR FILING DATE: 1998-04-29
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OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082569
OR FILING DATE: 1998-04-21
OR APPLICATION NUMBER: 60/082704
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OR APPLICATION NUMBER: 60/082804
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OR FILING DATE: 1998-04-08
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FILING DATE: 1998-04-15
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  VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
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RESULT 5
US-09-978-697-508
Sequence 508, Application US/09978697
Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Bakkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Betstein, David
APPLICANT: Betstein, David
APPLICANT: Betstein, David
APPLICANT: Ferrara, Napoleon
APPLICANT: Fivaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Goo, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gerritsen, Mary E.
APPLICANT: Gooddard, Audrey
APPLICANT: Goodwski, Paul J.
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CURRENT APPLICATION | CURRENT FILING DATE:
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DR FILING DATE: 1998-03-30

DR APPLICATION NUMBER: 60/080105

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080107

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080165

DR FILING DATE: 1998-03-31

DR APPLICATION NUMBER: 60/080194

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APPLICATION NUMBER: 60/065311
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Kljavin,
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Wood, William I
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PATENT NO. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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: Botstein, David
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CURRENT APPLICATION NUMBER: US/09/978,192A

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CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR FILING DATE: 1997-11-31

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PRIOR APPLICATION NUMBER: 60/07450

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PRIOR APPLICATION NUMBER: 60/077641

PRIOR PILING DATE: 1998-03-11

PRIOR PRILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER: 60/07764

PRIOR APPLICATION NUMBER: 60/07886

PRIOR APPLICATION NUMBER: 60/07886

PRIOR APPLICATION NUMBER: 60/078936

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OR APPLICATION NUMBER: 60/079689
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079663
OR APPLICATION NUMBER: 60/079728
OR APPLICATION NUMBER: 60/079728
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079786
OR APPLICATION NUMBER: 60/079780
OR APPLICATION NUMBER: 60/079920
OR APPLICATION NUMBER: 60/079920
OR APPLICATION NUMBER: 60/079920
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APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
FILING DATE: 1998-03-27
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Kuo, Sophia S.
Napier, Mary A.
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Grimaldi,
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Timothy A.
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NUMBER: 60, : 1998-03-3:

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APPLICATION NUMBER: FILING DATE: 1998-0

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APPLICATION NUMBER: 60/080165

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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081071

APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/081370

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APPLICATION NUMBER: 60/081195
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OR FILING DATE: 1998-05-06
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OR APPLICATION NUMBER: 60/084640
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Pred. No. 1.5e-114;
Mismatches 0;
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OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081229
OR FILING DATE: 1998-04-09
OR APPLICATION NUMBER: 60/081955
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081817
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OR APPLICATION NUMBER: 60/081820
OR APPLICATION NUMBER: 60/081952
OR FILING DATE: 1998-04-15
OR APPLICATION NUMBER: 60/081952
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PRIOR PRIOR

APPLICATION NUMBER:

60/083496

DR FILING DATE: 1998-04-23

OR APPLICATION NUMBER: 60/083336

DR PILING DATE: 1998-04-27

DR APPLICATION NUMBER: 60/083322

DR FILING DATE: 1998-04-28

DR APPLICATION NUMBER: 60/083392

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DR APPLICATION NUMBER: 60/083499

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DR APPLICATION NUMBER: 60/083545

DR FILING DATE: 1998-04-29

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DR APPLICATION NUMBER: 60/083558

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DR FILING DATE: 1998-04-29

OR APPLICATION NUMBER: 60/083559

OR APPLICATION NUMBER: 60/083559

OR FILING DATE: 1998-04-29

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FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082796

NA APPLICATION NUMBER: 60/082704
NR FILING DATE: 1998-04-22
NR APPLICATION NUMBER: 60/082804
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NR APPLICATION NUMBER: 60/082700
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NR FILING DATE: 1998-04-27
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APPLICATION NUMBER: 60/081838 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/082568 FILING DATE: 1998-04-21 FILING DATE: 1998-04-21 FILING DATE: 1998-04-21

US-09-978-192A-508

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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P
APPLICANT: Botstein, Dav
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C9
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DR FILING DATE: 1997-11-03
DR APPLICATION NUMBER: 60/065311
DR FILING DATE: 1997-11-13
DR APPLICATION NUMBER: 60/066364
DR FILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/077450
                                                 APPLICATION NUMBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
                                                                                                                      APPLICATION NUMBER: 60/078939
FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079294
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FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/078886
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FILING DATE: 1998-0:
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APPLICATION NUMBER: 60/078910
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APPLICATION NUMBER: 60/077649
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APPLICATION NUMBER: 60/077632
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NO. US20020177553A1
LINFORMATION:
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Botstein, David
Desnoyers, Luc
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Shelton, David L.
Stewart, Timothy A.
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Hillan, Kenneth J
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Godowski, Paul J.
Grimaldi, J. Christopher
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Filvaroff, Ellen
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Sophia S.
                                                                                                                                                                                                                                                                                                                                                 NUMBER: 60/077791
                                  1998-03-27
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                   60/079689
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PRIOR RIOR PRIOR OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080328
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/080333
OR FILING DATE: 1998-04-01
OR FILING DATE: 1998-04-01
OR APPLICATION NUMBER: 60/081070
OR APPLICATION NUMBER: 60/081070
OR APPLICATION NUMBER: 60/081070
OR FILING DATE: 1998-04-08
OR APPLICATION NUMBER: 60/081049
OR APPLICATION NUMBER: 60/081071
OR APPLICATION NUMBER: 60/081071
OR APPLICATION NUMBER: 60/081071 R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/00
RR APPLICATION NUMBER: 60/00
RR FILING DATE: 1998-04-09
RR FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/083392 FILING DATE: 1998-04-29 APPLICATION NUMBER: 60/083495 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/ FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083496
FILING DATE: 1998-04-29 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082797 FILING DATE: FILING DATE: 1998-04 APPLICATION NUMBER: APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/082804 FILING DATE: 1998-04-15 APPLICATION NUMBER: 60/081952 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082569 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081955 FILING DATE: 1998-04-21 APPLICATION NUMBER: 60/082568 FILING DATE: APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/081819 FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/080327 APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-31 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079920 FILING DATE: 1998-03-30 FILING DATE: 1998-03 APPLICATION NUMBER: FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079786 APPLICATION NUMBER: 60/ FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/0,79728 NUMBER: 60/083499 1998-04-23 1998-04-22 1998-04-1 1998-04-15 1998-04-15 1998-04-15 1998-03-31 1998-03-30 1998-03-3 60/082796 60/082700 60/081838 60/081195 60/081817 60/081229 60/081203 60/080165 60/079923 60/079663

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Best Local Similarity
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FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085697
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APPLICATION NUMBER: 60/085573
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FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085338
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APPLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/083742
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GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C3
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/
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Hillan, Kenneth J
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J. Christopher
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                                                       MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
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CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
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                  PRIOR PRIOR
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Stewart, Timothy A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/91885
PRIOR FILING DATE: 2001-07-30.
PRIOR FILING DATE: 2001-07-30.
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/06249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/06311
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06364
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Best Local Similarity
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Baker Kevin P.
Botstein, David
Desnoyers, Luc
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Shelton, David L.
Stewart, Timothy A.
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Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Filvaroff,
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f, Ellen
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Pred. No. 1.5e-114;
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PREPLICATION NUMBER: 60/080327

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OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080333

OR FILING DATE: 1998-04-01

OR APPLICATION NUMBER: 60/080334

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OR APPLICATION NUMBER: 60/081071

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OR APPLICATION NUMBER: 60/08129

OR APPLICATION NUMBER: 60/081819

R FILING DATE: 1998-03-20
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DR FILING DATE: 1998-03-25
DR APPLICATION NUMBER: 60/079656
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DR APPLICATION NUMBER: 60/079664
DR FILING DATE: 1998-03-27
DR APPLICATION NUMBER: 60/079669 APPLICATION NUMBER: 60/080165 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080194 FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079786
EILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079920 APPLICATION NUMBER: 60/080105 FILING DATE: 1998-03-31 APPLICATION NUMBER: 60/080107 FILING DATE: 1998-03-31 FILING DATE: 1998-03-30
APPLICATION NUMBER: 60/079923 FILING DATE: 1998-03-27 APPLICATION NUMBER: 60/079663 NUMBER: 60/079728 NUMBER: 60/078886 NUMBER: 60/077791 NUMBER: 60/077649: 1998-03-11 1998-03-27 1998-03-30 1998-03-20 1998-03-10 1998-03-20 60/078910 60/078939 60/078936 60/078004 60/077632 60/077641

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OR APPLICATION NUMBER: 60/08
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APPLICATION NUMBER: 60/ FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/ 60/084441 60/084414 60/084366

FILING DATE: 1998-05-06
APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
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APPLICATION N NUMBER: 1998-05-07 60/084640 60/084639 60/084637

FILING DATE: APPLICATION NUMBER: NUMBER: 1998-05-1998-5-07 1998-05-07 60/084627 60/084600 60/084598

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               TITLE OF INVENTION: Acids Encoding the S. FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
                                                              APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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APPLICANT: Baker Kev
APPLICANT: Botstein,
         PRIOR
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R APPLICATION NUMBER: 60/085580
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Baker Kevin P.
Botstein, David
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Cao, Wei-Qiang
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APPLICATION NUMBER: 60/077641
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OR APPLICATION NUMBER: 60/081819
OR APPLICATION NUMBER: 60/081952
OR APPLICATION NUMBER: 60/081952
                                                                                                                                                 DR APPLICATION NUMBER: 60/084598
DR FILING DATE: 1998-05-07
DR APPLICATION NUMBER: 60/084600
DR FILING DATE: 1998-5-07
DR APPLICATION NUMBER: 60/084627
DR FILING DATE: 1998-05-07
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DR APPLICATION NUMBER: 60/083742
DR FILING DATE: 1998-04-30
DR PRICATION NUMBER: 60/084366
DR FILING DATE: 1998-05-05
DR APPLICATION NUMBER: 60/084414
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R APPLICATION NUMBER: 60/08
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RR APPLICATION NUMBER: 60/082569

RR FILING DATE: 1998-04-21

DR APPLICATION NUMBER: 60/082704

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DR APPLICATION NUMBER: 60/082804

DR FILING DATE: 1999-04-22

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APPLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/083392
FILING DATE: 1998-04-29
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FILING DATE: 1998-05-07
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083500
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APPLICATION NUMBER: 60/083322
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
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FILING DATE: 1998-04-22
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OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085580
OR FILING DATE: 1998-05-15,
OR APPLICATION NUMBER: 60/085573
OR FILING DATE: 1998-05-15
OR APPLICATION NUMBER: 60/085704
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FILING DATE: 1998-05-13
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VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                         GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                           GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                                            GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                           ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP 120
                     VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                                                                                 GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
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60

240

240

180

120

180

RESULT 12 US-09-978-608A-506 Sequence 506, Application 1
Publication No. US20030045GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Grimaldi, J. Christopher Gurney, Austin L. Hillan, Kenneth J Kijavin, Ivar J. Kuo, Sophia S. Namior Fong, Roy, Margaret Ann Shelton, David L. Stewart, Timothy i Gerritsen, Mary Goddard, Audrey Ferrara, Napoleon Filvaroff, Ellen Paoni, Pan, James; Napier, Mary A. Godowski, Paul Gerber, Hanspeter Botstein, David Desnoyers, Luc Baker Kevin Eaton, Application US/09978608A US20030045462A1 Wei-Qiang Sherman Dan Nicholas Mary יסי. 4 Ħ

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RESULT 13
US-09-978-608A-508
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SEQ ID NO 506
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
                  APPLICANT:
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C22
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     INVENTION:
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                Williams, P. Mickey Wood, William I.
                                                                                                             Paoni,
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Desnoyers, Luc
                                                                             Shelton,
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Grimaldi, J. Christopher
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Gerritsen, Mary E.
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                                               Stewart, Timo
Tumas, Daniel
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Hillan, Kenneth J
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                                                                                                             James;
i, Nicholas F.
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                                                            David L.
   Secreted and
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 Transmembrane
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Polypeptides and Nucleic
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RESULT 14
US-09-978-585A-506
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APPLICANT: Ashkenaz
APPLICANT: Baker K
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Prior Application removed
SEQ ID NO 508
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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C15
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TYPE: PRT
ORGANISM: Hómo:
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FILE REFERENCE: P2630P1022
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
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Similarity 100.0%; F
73; Conservative 0;
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Botstein, David
Desnoyers, Luc
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Gurney, Austin L.
Hillan, Kenneth J
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Filvaroff, Ellen
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Godowski, Paul
                                                                                                                                                           Paoni,
                                                                                                                                                                           Pan, James;
                                                                                                                                                                                            Napier, Mary A.
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Kuo, Sophia S.
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                                                                                                                                                           Nicholas F.
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Pred. No. 1.5e-114;
; Mismatches 0;
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RESULT 15
US-09-978-585A-508
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NUMBER OF SEQ ID NOS: 624
Prior Application removed -
SEQ ID NO 506
LENGTH: 273
CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrappe
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                                                                                                                                             APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
                                                            APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C15
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                                                                                                                                         Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Kuo, Sophia S.
Napier, Mary A.
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Gerritsen, Mary E.
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Desnoyers, Luc
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Search completed: September 10, 2003, 17:24:42 Job time : 63 secs

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Maximum DB
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1.

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1505
1 MRGSQEVLLMWLLVLAVGGT......
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       328717 seqs, 42310858 residues
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US-09-349-697A-19
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US-09-363-316B-34
US-09-363-316B-4
US-09-363-316B-3
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US-09-363-316B-3
US-09-467-997-1
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00 QV QV QV	Que Bes Mat Qy Db Db	RESUIUS-00 VS-00 V		
120 PGRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVP	Query Match 78.4%; Score 1180; DB 4; Length 278; Best Local Similarity 77.7%; Pred: No. 1e-86; Matches 213; Conservative 19; Mismatches 40; Indels 2; Gaps Matches 213; Conservative 19; Mismatches 40; Indels 2; Gaps	RESULT 1 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 US-09-724-864-52 RESULT IN US-09-724-864 CURRENT APPLICATION NUMBER: US-09-724-864 CURRENT APPLICATION NUMBER: US-09-724-864 CURRENT FILING DATE: 2000-11-28 PRIOR APPLICATION NUMBER: US-09-724-864 CURRENT FILING DATE: 199-12-23 NUMBER OF SEQ ID NOS: 72 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 52 LENGTH: 278 TYPE: PRT ORGANISM: Mouse	182 12.1 810 4 US-09-976-165-34 Sequence 34 175.5 11.7 2321 4 US-09-976-230-652-2 Sequence 2, 175 11.6 652 2 US-08-751-305-2 Sequence 2, 175 11.6 2703 1 US-08-185-432-19 Sequence 19 ALIGNMENTS	47-1 Sequence 1, 53-1 Sequence 1, 66B-1 Sequence 1, 70A-37 Sequence 37 99-37 Sequence 37 68-37 Sequence 37 68-37 Sequence 37 56B-37 Sequence 37 56B-37 Sequence 34 99-34 Sequence 34 99-34 Sequence 34 99-34 Sequence 34 Sequence 34 Sequence 34
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RESULT 2 US-09-249-697A-6 ; Sequence 6, Application US/09249697A

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; NAME/KEY: misc feature
; LOCATION: (357)
; OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-6
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APPLICANT: Yeung, George
TITLE OF INVESTION: EGF MOTIF PROTEIN MATERIA
FILE REFERENCE: 28110/35852
CURRENT APPLICATION NUMBER: US/09/363,316B
CURRENT FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 09/249,697
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NAME/KEY: VARIANT
LOCATION: (1)...(553)
OTHER INFORMATION: Xaa = Any Amino Ac
                                                              Matches
                                                                              Query Match
Best Local &
                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application Patent No. 6392019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 08/968,800 PRIOR FILING DATE: 1997-11-22
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TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
TITLE OF INVENTION: LIVER SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ford, John APPLICANT: Yeung, Geo
                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   159 YWCQCWEGHSLSADGTLCV----
39 PVSESFVQRVYQPFLTTCDGHRACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGL |: | : | | | | : | : | | | | | : | |
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                                                          ch 16.9%;
1 Similarity 34.5%;
60; Conservative 2
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                                                        21;
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                                                          Score 254.5; DB 4;
Pred. No. 1.4e-12;
1; Mismatches 62;
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Pred. No. 1.4
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                                                                                           Length
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; ORGANISM: Homo sapiens
US-09-249-697A-19
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US-09-249-697A-19
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                                   APPLICANT: Yeung, George
TITLE OF INVENTION: LOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
TITLE OF INVENTION: LIVER SPLEEN
FILE REFERENCE: 24011-727
CURRENT APPLICATION NUMBER: US/09/249,697A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
NUMBER OF SEO ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 3.0
TYPE: PRT
TYPE: PRT
                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Yeung, Geo
                                                                                                                                                                                                                                                                                                                                         Sequence 19, Application US/09249697A Patent No. 6392018
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SEQ ID NO 389
LENGTH: 284
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Best Local Similarity
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APPLICANT:
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APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
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5. 6573095
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRC 125
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Pred. No. 9.3e-13;
5; Mismatches 51
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US-09-363-316B-18
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; ORGANISM: Homo sapiens
US-09-363-316B-24
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FILE REFERENCE: 28110/35852
CURRENT APPLICATION NUMBER: US/09/363,316B
CURRENT FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 09/249,697
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ford, John
APPLICANT: Yeung, Geo
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Best Local Similarity
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Best Local Similarity
Matches 57; Conser
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                                                                               APPLICANT: Yeung, George
TITLE OF INVENTION: EGF MOTE PROTEIN MATERIALS AND METHODS
FILE REFERENCE: 28110/35852
CURRENT APPLICATION NUMBER: US/09/363,316B
CURRENT FILING DATE: 1999-07-28
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PRIOR APPLICATION NUMBER: US 09/249,697
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                       VGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGSYKCFCLSGHMIMPDAT-CV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.7%; Score 251.5; DB 4; 36.8%; Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PKGGPP-----RVAPN 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.7%; Score 251.5; DB 4; 36.8%; Pred. No. 2.4e-12; tive 17; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOTIF PROTEIN MATERIALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50;
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; NAME/KEY: VARIANT
; LOCATION: (1)...(537)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-4
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US-09-249-697A-4
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, NAME/KEY: misc feature
; LOCATION: (501-502)
; OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-18
                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 4
                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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SOFTWARE: FASTSEQ for Windows
SEQ ID NO 18
LENGTH: 502
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 08/968,800 PRIOR FILING DATE: 1997-11-22 NUMBER OF SEQ ID NOS: 19
SOFTWARE: FARTCER OF US 197-11-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILE REFERENCE: 24011-727
CURRENT APPLICATION NUMBER: US/09/249,697A
CURRENT FILING DATE: 1999-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Yeung, George
TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM
TITLE OF INVENTION: LIVER SPLEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ford, John APPLICANT: Yeung, Geo
                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 537
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                      Local Similarity 39.3%;
les 48; Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / MALCN 14.4%;
Local Similarity 39.3%;
les 48; Conservative 1
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116 PN 117
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                                                                                                                                                                         91 GWKRTSGLPGACGAAICQPPCKNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 RCVNTHGSYKCFCLSGHMLMPDAT-CVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLA 115
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                                   PN 188
                                                                    RCVNTHGSYKCFCLSGHMLMPDAT-CVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLA 115
                                                                                                      RCINTAGSYWCQCWEGHSLSADGTLCV--
                                                                                                                                         GWRRNS--KGVC-EATCEPGCK-FGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQH 56
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                                                                                                                                                                                                            Score 216.5; DB 4;
Pred. No. 1.4e-09;
0; Mismatches 35;
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Pred. No. 1.3e-09;
0; Mismatches 35
                                                                                                                                                                                                                                             DB 4;
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                                                                                                      -PKGGPP-----RVA 186
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                                                                                                                                                                                                              29;
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RESULT

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TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIA
FILE REFERENCE: 2810/35852
CURRENT APPLICATION NUMBER: US/09/363,316B
CURRENT FILLING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: US 09/249,697
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1997-11-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 4
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                                                                                                                                                        ; TYPE: PRT; ORGANISM: Homo sapiens US-09-249-697A-3
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US-09-249-697A-3
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; Sequence 4, Application US/09363316B
; Patent No. 6392019
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                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09249697A Patent No. 6392018
GENERAL INFORMATION:
                                                                                              Query Match
Best Local Similarity
                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ford, John
APPLICANT: Yeung, George
TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
TITLE OF INVENTION: LIVER SPLEEN
FILE REFERENCE: 24011-727
                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 08/968,800 PRIOR FILING DATE: 1997-11-22 NUMBER OF SEQ ID NOS: 19
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CURRENT FILING DATE: 1999-02-12
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NAME/KEY: misc_feature
LOCATION: (503)
OTHER INFORMATION: Xaa = any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 537
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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                                91 GWKRTSGLPGACGAAICQPPCRNGGSCVQPGRCRCPAGWRGDTCQSDVDECSARRGGCPQ 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 RCVNTHGSYKCFCLSGHMLMPDAT-CVNSRTCAMINCQYSCEDTEEGPQCLCPSSGLRLA 115
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GWRRNS--KGVC-EATCEPGCK-FGECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQH 56
                                                                                  Conservative
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                                                                                                  14.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10; Mismatches
                                                                                              Score 215.5; DB 4
Pred. No. 2.5e-10;
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Pred. No. 1.4e-09;
                                                                              Mismatches
                                                                                                                DB 4;
                                                                              32;
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                                                                                                                Length 100;
                                                                              Indels
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US-09-363-316B-3
                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09467997 Patent No. 6379925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/249,697
PRIOR FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 08/968,800
PRIOR FILING DATE: 1997-11-22
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PASESEQ for Windows Version 3.0
SEQ ID NO 3
                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn Ver
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kitajewski, Jan
APPLICANT: Uyttendaele, Hendrik
TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
FILE REFERENCE: 53863-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/467,997
CURRENT FILING DATE: 1999-12-20
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APPLICANT: Yeung, George
TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 28110/35852
CURRENT APPLICATION NUMBER: US/09/363,316B
CURRENT FILING DATE: 1999-07-28
                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                           LENGTH: 1964
                                                                                                                                                                                                  Local Similarity
nes 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.3%;
Local Similarity 48.3%;
es 42; Conservative
                                 190 RDINECFLEPGPCPQGTSCHNTLGSYQCLCPVGQEGPQCKLRKGACPPGSCLNGGTCQLV 249
                                                                       136 SDVDECSARRGGCPQ--RCINTAGSYWCQC---WEGHSLSADGTLCVP----KGGPPRVA 186
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                                                                                                               ASGRPQCSCEPGWTGEQCQLRDFCSA----NPCANGGVCLATYPQIQCRCPPGFEGHTCE 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCINTAGSYWCQCWEGHSLSADGTLCV 177
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                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                13.0%; Score 196; DB 4; I
34.2%; Pred. No. 2.7e-07;
rative 12; Mismatches 54;
-TGVDSAMKEE 199
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Pred. No. 2.5e-10;
"" matches 32;
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                                                                             Sequence 2, Application US/08435434
PATENT NO. 5714385
GENERAL INFORMATION:
APPLICANT: Mather, Jennie P.
APPLICANT: Li, Ronghao
APPLICANT: Chen, Jian
TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS
NUMBER OF SEQUENCES: 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
INFORMATION FOR SEQ ID NO:
$EQUENCE CHARACTERISTICS:
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Stimulating Factor for the AXL Receptor NUMBER OF SEQUENCES: {\tt 4}
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                              STREET:
                                                  ADDRESSEE:
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STATE: California
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         SEE: Genentech, Inc.
: 460 Point San Bruno Blvd
South San Francisco
                                                                                                                                                                                                                                                                                                                                                               KNSGFATCVQNLPDQC----TPNPCDRKGTQACQDLMGNFFCLCKAGWGGRLCDKDVNEC 160
                                                                                                                                                                                                                                                                                            SQENGGCLQICHNKPGSFHCSCHSGFELSSDGRTC 195
                                                                                                                                                                                                                                                                                                                            SARRGGCPORCINTAGSYWCOCWEGHSLSADGTLC 176
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1840 Dehavilland Drive
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Manfioletti, Guidalberto
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Avanzi, Giancarlo
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Patent No. 5721139
GENERAL INFORMATION:
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                                COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,436
APPLICATION NUMBER: US/08/435,436
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NIMBER
                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                              APPLICANT: Mather, Jennie P. APPLICANT: Li, Ronghao APPLICANT: Chen, Jian
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                 STREET: 460 Point San Bruno CITY: South San Francisco STATE: California
FILING DATE: 1
CLASSIFICATION:
                                                                                                                                                                 ZIP: 94080
                                                                                                                                                                              COUNTRY:
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REGISTRATION NUMBER: 00
REFERENCE/DOCKET NUMBER:
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                                US/08/435,436
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Pred. No. 2.9e-07;
8; Mismatches 64
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                                                                                                                         floppy disk
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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/ACENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELECOMMUNICATION INFORMATION:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*

2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*

3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*

4: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
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Gapop 10.0 , Gapext 0.5
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Result	Score	74	Length DB	DB		Description
1	1505	100.0	273	20	AAY41769	Human PRO213-1 pro
2	1505	100.0	273	20	AAY41770	Human PRO1330 prot
ω	1505	100.0	273	21	AAB44325	
4.	1505	100.0	273	21	AAB44326	Human PRO1330 prot
σ	1505	100.0	273	21	AAB18673	Amino acid sequenc
D	1505	100.0	273	21	AAB18674	Amino acid sequenc
7	1505	100.0	273	21	AAB24042	Human PRO213 prote
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98US-0080105. 98US-0080107. 98US-0080165. 98US-0080194. 98US-0080327. 98US-0080333. 98US-0080333.

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98US-0079689. 98US-0079728. 98US-0079786. 98US-0079920. 98US-0079923.

98US-0078939. 98US-0079294. 98US-0079656. 98US-0079663.

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                          Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disord secreted protein; transmembrane protein.
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N-PSDB; AAZ34311.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
                                                                                                                                                                                                                                                                                          Sequence
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DB; AAZ34312.
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                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                              ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                            MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                                   GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSSLL
                                                                                                                GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                             MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
                                                                                                   GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                  ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                       GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
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                                                                                                                                                                                                                                          100.0%;
ilarity 100.0%;
Conservative 0
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98US-0085689

98US-0085689

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Pred. No. 5
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02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
30-DEC-1999;
05-JAN-2000;
06-JAN-2000;
                AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                                   Goddard
Kljavin
                                                                                                                                                                                                        Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
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29-OCT-1999;
                                                                                                                                                                                   Claim 12;
                                                                                                                                                                                                                                                                 WPI; 2000-611443/58.
N-PSDB; AAC78585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-NOV-1999;
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23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-APR-1999;
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21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC.
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N, Filvaroff E,
A, Godowski PJ,
IJ, Kuo SS, Nap
DL, Stewart TA,
                                                                                                                                                                                Fig 213; 636pp; English.
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; 2000WO-US00219.
; 2000WO-US00277.
; 2000WO-US00376.
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99WO-US30095.
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99US-0134287.
99US-0141037.
99US-0145698.
99US-0162506.
99WO-US28313.
99WO-US28551.
                                                                                                                                                                                                                                                                                                     Napier MA,
TA, Tumas D,
                                                                                                                                                                                                                                                                                                 Botstein D, Desnoyers L, Eaton DL;
Fong S, Gao W, Gerber H, Gerritsen ME;
Grimaldi CJ, Gurney AL, Hillan KJ;
ier MA, Pan J, Paoni NF, Roy MA;
Tumas D, Williams PM, Wood WI;
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Sequence

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AAB44326
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AXX AAB4
AXX AAB4
AXX O8-F
XX O8-F
XX Huma
XX Homo
XX Homo
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XX Homo
PN W020
XX Homo
PN 12-F
XX 08-M
PR 12-M
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Best Local Similarity
Matches 273; Conserv
                 Ashkenazi AJ, Baker KP,
Ferrara N, Filvaroff E,
Goddard A, Godowski PJ,
Kljavin IJ, Kuo SS, Napp
Shelton DL, Stewart TA,
                                                                                                                                                                                                                                                                                                     30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
16-DEC-1999;
30-DEC-1999;
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29-OCT-1999
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14-MAY-1999
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21-APR-1999
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expressed sequence tag; detection; cancer;
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                                                                                                                                                              GENENTECH INC.
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2000WO-US00219.
2000WO-US00277.
2000WO-US00376.
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ilarity 100.0%;
Conservative (
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99WO-US30095.
99WO-US31243.
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99US-0123957
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                 KP, Botstein D, Desnoyers L, Eaton
E, Fong S, Gao W, Gerber H, Gerr
PJ, Grümaldi CJ, Gurney AL, Hillan
Napier MA, Pan J, Paoni NF, Roy M
TA, Tumas D, Williams PM, Wood WI;
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Pred. No. 5.5e-95;
D; Mismatches 0;
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                                Desnoyers L, L. The W, Gerber H, Gerritse... AL, Hillan KJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:508
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                                                                                         Gerritsen ME;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bloactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                                                                                                                                                       Growth arrest-specific gene 6 protein homologue; PRO320; PRO938; PRO10: PRO296; PRO213; PRO1449; angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder; endothelial disorder; angiogenic disorder; cancer; trauma; wound; artherosclerosis; cardiac hypertrophy.
 Modified-site
                              Modified-site
                                                         Modified-site
                                                                                                                                Homo
                                                                                                                                                                                                                                   Amino acid
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                                                                                                                                                                                                                                                                                                                          AAB18673
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cellular a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nove1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-611443/58
N-PSDB; AAC78586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC78458 to AAC78599 represent polynucleotide and EST (expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRO polypeptides and polynucleotides used in detection methods, rget bioactive molecules to specific cells, and to modulate lar activities -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
                                                                                                                                                                                                                                                                                                                                                                                                                VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                                                                                                                                                                                                               VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRGSQEVILMWILIVLAVGGTEHAYR ÞGRRVCAVRÁHGD ÞVSES FVQRVYQ ÞFLTTCDGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 215; 636pp; English
                                                                                                                                                                                                                                sequence of a human a PRO213 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences which encode secreted or transmembrane PRO
                           /note=
26..30
                                                         /note=
19..25
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                note=
                                                                                                                                                                                                                                                                                                                        Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRO polynucleotide sequences.
                "amidation site"
                                          "N-myristoylation
                                                                                                                                                                                                                                                                                                                          273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1505; DB 21; Pred. No. 5.5e-95;
                                                                     sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                          site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                      PRO938; PRO1031;
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REGERERAL AND COLOUR SERVICE AND

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Matches
                              Query Match
Best Local
                                                                                                                                                                    The present sequence represents PRO213, a human growth arrest-specific gene 6 protein homologue. The specification describes PRO320, PRO338, PRO2131, PRO2296, PRO2131,  PRO2131, PRO2131, PRO2131, PRO2131, PRO21311, PRO21311, PRO
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A composition useful for treatment and diagnosis of a cardiovascular, endothelial or angiogenic disorder, especially cancer, comprises (an agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213, PRO1330 or PRO1449 polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood
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14-MAY-1999;
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26-APR-1999;
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                                 Similarity
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                                                                                                                   273 AA;
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   100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10; 152pp; English
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99US-0130232.
99US-0131022.
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99US-0134287
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93..97
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191..197
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152..164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Goddard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CAMP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-myristoylation
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   0
Score 1505; DB 21
Pred. No. 5.5e-95;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          attachment sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Α,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gurney AL,
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                                                                                                                       Human; tumour; diagnosis; neoplastic disease; identification; cancer; tumourigenesis; detection; neoplastic cell growth; proliferation; cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder
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                                                                                                                                                                                                                                 Human PRO213
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Matches 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes an isolated antibody (Ab) that binds to one of the human proteins (P) designated PRO213, PRO1330, PRO1449, PRO237, PRO324, PRO351, PRO351, PRO531, PRO538, PRO518, PRO772, PRO372, PRO350, PRO3618, PRO474. The Ab can be used in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation in mammals, including humans. Genes and polypeptides encoded by them, that are amplified in the genome of a tumour cell, can be identified and are useful targets for the treatment and prevention of certain cancers and may be used to monitor tumour treatment. Compounds that inhibit the expression or activity of the identified polypeptides can be identified and used as antagonists. Benign or mallgnant tumours, inflammatory disorders and immunological disorders can be treated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-MAR-1999
12-MAR-1999
29-MAR-1999
21-APR-1999
21-APR-1999
05-CCT-1999
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02-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                              AAC58123 to AAC58224 represent hybridisation probes and PCR primers used in the isolation of the human PRO sequences. AAC58225 to AAC58241 and AAB24041 to AAB24056 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation in mammals, including humans, and in monitoring tumor treatment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 61; Fig 4; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPT; 2000-572269/53.
N-PSDB; AAC58226.
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 241
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                                                                                                                                                                                                                                                                                                                         Similarity
                 VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                         GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                           GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                      GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                      GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                      ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                                                             MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
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VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0130232
99US-0131445
99US-US23089
99WO-US28313
99WO-US28551
99WO-US28564
99WO-US31243
99WO-US312474
                                                                                                                                                                                                                                                                                                                                                                      AA;
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99US-0126773.
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99US-0123957
                                                                                                                                                                                                                                                                                                                     100.0%;
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Pred. No. 5.5e~95;
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Query Match
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Similarity

100.0%; ilarity 100.0%; Conservative 0

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Score 1505; DB 21; Pred. No. 5.5e-95; ; Mismatches 0;

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Gaps

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                                                 The present invention describes an isolated antibody (Ab) that binds to CC one of the human proteins (P) designated PRO213, PRO3130, PRO31449, CC PRO237, PRO324, PRO351, PRO3622, PRO615, PRO531, PRO538, PRO3664, PRO618, CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions and methods for the diagnosis and treatment of neoplastic cell growth CC and methods for the diagnosis and treatment of neoplastic cell growth can be identified and are useful targets for the treatment and prevention of CC certain cancers and may be used to monitor tumour treatment. Compounds CC that inhibit the expression or activity of the identified polypeptides CC can be identified and used as antagonists. Benign or malignant tumours, inflammatory disorders and immunological disorders can be treated. CANC58123 to AAC58224 represent hybridisation probes and PCR primers used in the isolation of the human PRO sequences. AAC5825 to AAC58241 and CC AAB24041 to AAB24056 represent human PRO polynuclectide and protein CC sequences given in the exemplification of the present invention.
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05-OCT-1999;
30-NOV-1999;
02-DEC-1999;
02-DEC-1999;
30-DEC-1999;
30-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated antibody for use in compositions and methods for the diagnosis and treatment of neoplastic cell growth and proliferation mammals, including humans, and in monitoring tumor treatment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-572269/53.
N-PSDB; AAC58227.
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12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61; Fig 6; 195pp; English.
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99WO-US28313.
99WO-US28551.
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99WO-US31274.
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99US-0130232.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ĽJ,
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RESULT 9
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This is the human TANGO 125 (T125) amino acid sequence. That two epidermal growth factor (EGF)-like domains at ami 107-134 and 141-176 and is predicted to have a molecular approximately 30kD. T125 is predicted to have no transmem
                                                                                                            WPI; 2000-013240/01.
N-PSDB; AAZ37131.
                                                       Claim 1; Fig
                                                                             cellular
                                                                                        Novel
                                                                                                                                            Holtzman
                                                                                                                                                                                     23-APR-1998;
23-APR-1999;
                                                                                                                                                                                                                                                              WO9954437-A2
                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                         TANGO 125; T125; alternative splice variant; EGF domain; antibody; secreted protein; agonist; antagonist; predictive medicine; treatment; forensic biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human TANGO
                                                                                                                                                                (MILL-) MILLENNIUM
                                                                                                                                                                                                                   23-APR-1999;
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                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                       Protein
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                                                                                                                                            DA;
                                                                            processes
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99US-0065363
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23..274
/label= TANGO_125
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                                                                                                                                                               BIOTHERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                     and polypeptides used
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Domain Protein

/note=

"Epidermal growth

factor domain

/note= "Human mature T125 protein" 107..134

Homo sapiens.

Peptide

Location/Qualifiers

/label= Signal_peptide

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RESULT 10
AAE21079
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Best Local
                                                                                                                                                                                                                              Human; haematopoiesis; clotting; kidney failure; wound healing; cancer; neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease; heart disorder; ischaemic heart disease; neuroprotective; vulnerary; cardiovascular disorder; ischaemic heart disease; immunosuppressive; glomerular disease; glomerulonephritis; uterine disorder; hyperplasia; fetal spleen; prostate disorder; inflammatory disease; Crohn's disease; proliferative disorder; gynaecological; haemostatic; antibacterial; proliferative disorder; gynaecological; haemostatic; antibacterial; systemic lupus erythematosus; immunodeficiency disorder; tranquilliser; hypotensive; tumour; injury; trauma; antianginal; vasotropic; antiulcer; hypotensive; theumatoid arthritis; cardiant; renal disorder; heapottoric; artiporyis; cheumatoid arthritis; cardiant; renal disorder; heapottoric; artiporyis; cardiant; renal disorder; heapottoric; artiporyis; cardiant; renal disorder; heapottoric; artiporyis; cardiant; renal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and appears to be a secreted protein. There are three alternatively spliced forms of the T125 gene: T125a, T125b and T125c (AAZ37122-Z37135). The sequences of all variants of T125a, T125b and T125c (DAZ37122-Z37135). The sequences of all variants of T125 are used in the invention to create antibodies which selectively bind to T125. The T125 polypeptide is used to modulate a variety of cellular processes. It can be used to produce fusion proteins. The protein may also be used to produce antibodies, and to identify T125 antagonists and agonists. The T125 polynucleotides, polypeptides, homologues and antibodies can be used in screening assays; predictive medicine; and methods of treatment of T125 associated disorders. The T125 polynucleotides can be used to express the protein; to detect T125 mRNA; to detect genetic alterations in the T125 gene; in forensic biology; and as a source of primers and probes.
                                                                                                                                                                                                  hepatotropic;
T125.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE21079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human T125 (TANGO-125) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VHSFQQLGRIDSLSEQISELEEQLGSCSCKKDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       273 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                 antipsoriatic; antiallergic; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Pred. No. 5.5e-95;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273;
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Domain

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μ
MRGSQEVLLMWLL.VLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
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Query Match Best Local Matches

273;

Conservative

0;

Score 1505; Pred. No. 5.5); Mismatches

5.5e-95; hes 0;

Indels Length

Gaps

0

WPI; 2002-172001/22. N-PSDB; ABK33624.

One hundred and twenty two nucleic acids encoding PRO polypeptides,

273; 0;

Similarity

100.0%;

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CC disorder characterised by their aberrant expression or activity. The CC antibodies are useful as modulating agents in regulating a variety of CC cellular processes e.g. cell proliferation and/or cell differentiation. CC TANGO-139 is useful for treating kidney defects such as kidney failure. CC TANGO-125 is useful in wound healing and for treating cancer. TANGO-110 cis useful for treating neoplasia, TANGO-177 or WDNM-2 is useful for CC treating cancer, are useful to treat pancreatic disorders, such as concentration of the brain. TANGO-125, 110, 175 molecules treat heart disorders, e.g., ischaemic heart disease, cardiovascular disorders, such as ischaemic chart disease. TANGO-139, 125, 110 and 175 molecules are useful to treat crenal (kidney) disorders, such as allowerular disease (e.g., acute and cc thronic glomerularonephritis), TANGO-175 is useful to treat expleen, e.g., the fetal spleen, associated diseases and disorder. TANGO-125 treats prostate disorders, such as inflammatory diseases, Crohn's cdisease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for creating proliferative disorders, inflammatory diseases, Crohn's cdisease and tumours. TANGO-139, 125, 110, 175 or WDNM-2 are useful for creating proliferative disorders, inflammatory disorders. TANGO-175, or WDNM-2 activity also include apoptotic disorders, relumented arthritis, systemic lupus erythematosus, insulin-dependent diabetes mellitus, clisorders, e.g., immunodeficiency disorders, viral cdisorders, e.g., immunodeficiency disorders, viral cdisorders, e.g., cancers and inflammatory control arthritis, control arthritis, control and proportic disorders and inflammatory control are useful control are useful control are useful control and proportic disorders in human tribates mellitus, control and proportic disorders in human tribates mellitus, control and proportic disorders in human tribates of the invention control and proportic disorders in human tribates of the invention control and the proportic and proportic activity disorders in hum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel TANGO polypeptides and nucleic acid molecules useful as modulating agents in regulating cellular processes and for diagnosing and treating heart, liver, lung, kidney, inflammatory and cellular proliferative disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JUL-1998;
23-APR-1999;
22-JUN-1999;
29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1998;
23-APR-1998;
22-JUN-1998;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to inhibit a proteinase activity, to modulate cell-cell interactions, naematopolesis and the ability to modulate clotting. Polypeptide and polynuclectide of the invention are useful for diagnosing and treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to nucleic acids encoding a variety of proteins human T139 (TANGO-139), T125 (TANGO-125), T110 (TANGO-110), murine T175 (TANGO-175), human T175 or murine WDNM-2, having diagnostic, preventive, therapeutic and other uses. Polypeptide of the invention has the ability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-303420/34.
N-PSDB; AAD33536.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) HOLTZMAN D A.
) GOODEARL A D J.
) MCCARTHY S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fig 4; 138pp; English.
  273
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A,
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98US-0065661.

98US-0102705.

98US-0124538.

99US-0298531.

99US-0337930.

99US-0363630.
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RESULT 11
AAU83680
             Baker KP,
Grimaldi
                                                                                                                                                                            28-NOV-2000;
01-DEC-2000;
                                                                                                                                                                                                                         24-AUG-2000;
15-SEP-2000;
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25-JUL-2000;
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25-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; PRO; tumour; lung cancer; colon cancer; breast cancer; prostate tumour; rectal tumour; liver tumour; pericyte cell proliferation; chondrocyte cell proliferation; tumour necrosis factor-alpha.
                                                                                                                              28-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                              (GETH )
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                                                              GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard; Protein;
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             Desnoyers
C, Gurney
                                                                                            2001US-0854
2001WO-US17
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2000US-0747259.
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2000US-000000P.
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2000WO-US20710.
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2000US-220666P.
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           ΑĽ,
             Gerritsen ME, Goddard
Smith V, Stephan JF,
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Godowski I
Itanabe CK,
                              PJ;
             Wood WI;
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RESULT 12
ABU61155
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                                                                                               Human; PRO polypeptide; secreted and transmembrane protein; immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia; cardiac insufficiency; nervous system disorder; kidney disorder; bone disorder; cartilage disorder; arthritis; tumour; wound healing; genetic disorder; cytostatic; antidiabetic; antiinflammatory;
   14-NOV-2002
                             US2002169284-A1.
                                                                                        genetic disorde
antiarthritic;
                                                                                                                                                                             Human
                                                                                                                                                                                                    08-MAY-2003
                                                                                                                                                                                                                                                    ABU61155 standard; Protein; 273 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for treating a PRO related disorder and for diagnosing tumours such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or liver tumour -
                                                     Homo sapiens
                                                                                                                                                                                                                              ABU61155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                         anti-tumour;
                                                                                                                                                                          polypeptide
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Pred. No. 5.5e-95;
; Mismatches 0;
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24-FEB-2000
02-MAR-2000
10-MAR-2000
21-MAR-2000
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17-MAY-2000
22-MAY-2000
02-JUL-2000
24-JUG-2000
              06-NOV-1998;
07-DEC-1998;
22-DEC-1998;
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07-OCT-1998;
02-NOV-1998;
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25-MAR 1998;
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13-NOV-1997;
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05-JAN-2000;
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06-JAN-2000;
11-FEB-2000;
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17-MAR-1998
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17-OCT-1997
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25-MAY-2001
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30-DEC-1999;
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14-MAY-1999;
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2001WO-US06520.
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2000WO-US00277.
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2000WO-US03565.
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2001WO-US21735.
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2000WO-US14042.
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2001WO-US17092.
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2000WO-US05004
81US-0267213.

98US-01040220.

98US-0105413.

98US-01168978.

98US-01168978.

98US-011697368.

98US-021054.

98US-0218817.

99US-0254465.
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98US-077632P.
98US-077649P.
98US-07791P.
98US-078886P.
98US-078886P.
98US-078930P.
98US-078939P.
98US-079294P.
98US-07956P.
98US-079664P.
98US-0797689P.
98US-079664P.
98US-079768P.
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97US-065311P.
97US-066364P.
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99WO-US30095.
99WO-US31243.
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99WO-US05028
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10-MAR-1999; 12-APR-1999; 14-MAY-1999;

99US-0265686. 99US-0284291. 99US-0311832.

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                                                                                                                                                                                                                                                                                    The present invention relates to the isolation of novel human PRO CC polypeptides, and the polynucleotide sequences encoding them. The PRO CC PRO polypeptides are useful for detecting other PRO polypeptides, for CC polypeptides are useful for detecting other PRO polypeptides, for CC linking bioactive molecules to cells expressing PRO polypeptides, CC for modulating biological activities of cells expressing PRO polypeptides, CC polypeptides, and for for identifying agonists or antagonists. The bioactive molecule maybe a toxin, radiolabel or antibody, and causes CC polypeptides or death of the cell. The PRO polypeptides are useful for treating immune disorders, diabetes or hyper- or hypo-insulinaemia, CC cardiac insufficiency, nervous system disorders, kidney disorders, CC cardiac insufficiency, nervous system disorders, and wound healing. CC bone and cartilage disorders or arthritis, tumours, and wound healing. CC polypuctice are useful as CC contisted to probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for CC canalysis of individuals with genetic disorders, and in gene therapy. ABUG1071-ABUG1164 represent the human PRO polypeptides of the
                                                                                                                             Query Match
Best Local S
Matches 273
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25-AUG-1999; 99US-0380138
25-AUG-1999; 99US-0380142.
08-NOV-2000; 2000US-0709238
27-NOV-2000; 2000US-0723749
20-DEC-2000; 2000US-0816744.
22-MAR-2001; 2001US-0816920.
10-MAY-2001; 2001US-0854280.
10-MAY-2001; 2001US-0854280.
01-JUN-2001; 2001US-0872035.
05-JUN-2001; 2001US-0872035.
14-JUN-2001; 2001US-0886342.
19-JUN-2001; 2001US-0886345.
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Kljavin
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                         Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies -
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N-PSDB; ABX92683.
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                                                                                                                                                                                                                                                                               invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ashkenazi
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                                                                                                                             273;
61
                              61
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                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENENTECH INC.
                                                             MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
                    ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP 120
ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
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Filvaroff E,
Godowski PJ,
Kuo SS, Napi
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TA, Tumas D,
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                                                                                                                             0;
                                                                                                                           Score 1505; DB 24;
Pred. No. 5.5e-95;
; Mismatches 0;
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30-NOV-1999;
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2000WO-US00277
2000WO-US00376
2000WO-US03565
2000WO-US034341
2000WO-US055004
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2000WO-US23710,
2000WO-US232678,
2000WO-US332678,
2001WO-US06520,
2001WO-US06520,
2001WO-US09552,
2001WO-US17092,
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99WO-US31274.
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17-MAR-1998
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22-DEC-1998
55-MAR-1999
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14-MAY-1999

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27-NOV-2000

20-DEC-2000

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Goddard
Kljavin
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20-JUN-2001;
29-JUN-2001;
09-JUL-2001;
                                   Novel secreted and transmembrane polypeptides and polynucleotides encoding them useful for treating cancer, kidney diseases, bone, cartilage disorders and immune deficiencies
                    Claim 12;
The present invention relates to the isolation
                                                                             N-PSDB;
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                                                                             ABX92684.
                   Fig
                                                                                                     , Baker KP, Botstein D, Desnoyers L, Eaton D; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen Godowski DJ, Grimaldi JC, Gurney AL, Hillan KJ; Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA; Stewart TA, Tumas D, Williams PM, Wood WI;
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98US-079728P

98US-0105413

98US-0118416

98US-018413

98US-0218517

99US-0254465

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Best Local S
Matches 273
                                                                                                                                                                                                                                                                                                                                                          Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
10-MAR-1998;
11-MAR-1998;
                                                                                                    08-MAR-1999;
                                                                                                                                                                      16-SEP-1999
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Matches 272
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26-APR-1999 AAW88381; AAW88381

(first entry)

standard;

Protein;

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11-MAR-1998;
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27-MAR-1998;
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31-MAR-1998;
31-MA

Human neuro-growth factor-like protein Zneul

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contraception, or to regenerate nerves. LLAINCU LLUCI POLYPEPTIDES (see also AAW88382-97), including specific domains of Zneul and epitope-bearing portions of Zneul, can be used to raise specific antibodies for use e.g. in diagnostic assays.
                                                                                                                                                               EGF-like domains and may be involved in EGF receptor pathways. Zneul is widely expressed in adult tissues, with high expression in heart, placenta, spleen, testis, thyroid, spinal cord and lymph node. Zneul polypeptide can be used as a growth, maintenance, or differentiation factor in the spinal cord, heart, spleen, testis, thyroid and lymph nodes. It may also play a role in breast cancer, glioblastomas, and pituitary adenomas. Zneul may be used to treat Alzheimer's disease, cancer, to repopulate blood cells after chemotherapy, to stimulate myofibroblast proliferation, stimulate or inhibit growth factors made in the placenta, in fertility and
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This polypeptide comprises human Zneul, a new neuro-growth factor-like protein. Its amino acid sequence was deduced from the nucleotide sequence (see AAV84341) of a cDNA clone isolated from a brain cDNA library. Zneul's closest human homologue is HSMHC3W5A, a gene in the HLA class III region, which is contained in a cosmid which contains Notch 4. Zneul is also homologous to Notch 4 in it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .8-JUN-1998;
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273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jelinek LJ,
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0878322.
97US-0050143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US12763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= ",
136. 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105..135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "hydrophilic domain (HSM1), homologous to
an HSMHC3W5A domain "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note= "epidermal growth factor-like domain 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "putative signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides - used to, e.g. treat Alzheimer's to repopulate blood cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "epidermal growth factor-like domain 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zneul is also homologous to Notch 4 in its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lehner JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sheppard PO;
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Query Match Best Local Similarity

99.9%;

Score 1504; DB 20; Pred. No. 6.4e-95;

Length 273;

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Matches
                                                                   181
 241
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                                                                                            GPPRVAPNPTGVDSAMKEBVQRLQSRVDLLBEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                                                      GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCINTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                                                          ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                                                                                                                 MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                               VHSFQQLGRIDSLSEQISFLEEQLGSCSCKKDS
                                                               GPPRVAPNPTGVDSAMKEEVQRLQSRVDLLEEKLQLVLAPLHSLASQALEHGLPDPGSLL
                                                                                                                                   GRCRCPAGWRGDTCQSDVDECSARRGGCPQRCVNTAGSYWCQCWEGHSLSADGTLCVPKG
                                                                                                                                                                                                    ACSTYRTIYRTAYRRSPGLAPARPRYACCPGWKRTSGLPGACGAAICQPPCRNGGSCVQP
                                                                                                                                                                                                                                                                      MRGSQEVLLMWLLVLAVGGTEHAYRPGRRVCAVRAHGDPVSESFVQRVYQPFLTTCDGHR
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                                                                                                                                                                                                                                                                                                                                        Mismatches
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